```
        10         20         30         40         50         60
CATCATCAATAATCTACAGTACACTGATGGCAGCGGTCCAACTGCCAATCATTTTTGCCA

        70         80         90        100        110        120
CGTCATTTATGACGCAACGACGGCGAGCGTGGCGTGCTGACGTAACTGTGGGGCGGAGCG

       130        140        150        160        170        180
CGTCGCGGAGGCGGCGGCGCTGGGCGGGGCTGAGGGCGGCGGGGGCGGCGCGCGGGGCGG

       190        200        210        220        230        240
CGCGCGGGGCGGGGCGAGGGGCGGAGTTCCGCACCCGCTACGTCATTTTCAGACATTTTT

       250        260        270        280        290        300
TAGCAAATTTGCGCCTTTTGCAAGCATTTTTCTCACATTTCAGGTATTTAGAGGGCGGAT

       310        320        330        340        350        360
TTTTGGTGTTCGTACTTCCGTGTCACATAGTTCACTGTCAATCTTCATTACGGCTTAGAC

       370        380        390        400        410        420
AAATTTTCGGCGTCTTTTCCGGGTTTATGTCCCCGGTCACCTTTATGACTGTGTGAAACA

       430        440        450        460        470        480
CACCTGCCCATTGTTTACCCTTGGTCAGTTTTTTCGTCTCCTAGGGTGGGAACATCAAGA

       490        500        510        520        530        540
ACAAATTTGCCGAGTAATTGTGCACCTTTTTCCGCGTTAGGACTGCGTTTCACACGTAGA

       550        560        570        580        590        600
CAGACTTTTTCTCATTTTCTCACACTCCGTCGTCCGCTTCAGAGCTCTGCGTCTTCGCTG

       610        620        630        640        650        660
CCACCATGAAGTACCTGGTCCTCGTTCTCAACGACGGCATGAGTCGAATTGAAAAAGCTC
     MetLysTyrLeuValLeuValLeuAsnAspGlyMetSerArgIleGluLysAlaL

       670        680        690        700        710        720
TCCTGTGCAGCGATGGTGAGGTGGATTTAGAGTGTCATGAGGTACTTCCCCCTTCTCCCG
euLeuCysSerAspGlyGluValAspLeuGluCysHisGluValLeuProProSerProA

       730        740        750        760        770        780
CGCCTGTCCCCGCTTCTGTGTCACCCGTGAGGAGTCCTCCTCCTCTGTCTCCGGTGTTTC
laProValProAlaSerValSerProValArgSerProProProLeuSerProValPheP

       790        800        810        820        830        840
CTCCGTCTCCGCCAGCCCCGCTTGTGAATCCAGAGGCGAGTTCGCTGCTGCAGCAGTATC
roProSerProProAlaProLeuValAsnProGluAlaSerSerLeuLeuGlnGlnTyrA

       850        860        870        880        890        900
GGAGAGAGCTGTTAGAGAGGAGCCTGCTCCGAACGGCCGAAGGTCAGCAGCGTGCAGTGT
rgArgGluLeuLeuGluArgSerLeuLeuArgThrAlaGluGlyGlnGlnArgAlaValC

       910        920        930        940        950        960
GTCCATGTGAGCGGTTGCCCGTGGAAGAGGATGAGTGTCTGAATGCCGTAAATTTGCTGT
ysProCysGluArgLeuProValGluGluAspGluCysLeuAsnAlaValAsnLeuLeuP
```

FIGURE 1-1

```
      970        980        990       1000       1010       1020
TTCCTGATCCCTGGCTAAATGCAGCTGAAAATGGGGGGTGATATTTTTAAGTCTCCGGCTA
hePro AspProTrpLeuAsnAlaAlaGluAsnGlyGlyAspIlePheLysSerProAlaM

      1030       1040       1050       1060       1070       1080
TGTCTCCAGAACCGTGGATAGATTTGTCTAGCTACGATAGCGATGTAGAAGAGGTGACTA
etSerProGluProTrpIleAspLeuSerSerTyrAspSerAspValGluGluValThrS

      1090       1100       1110       1120       1130       1140
GTCACTTTTTTCTGGATTGCCCTGAAGACCCCAGTCGGGAGTGTTCATCTTGTGGGTTTC
erHisPhePheLeuAspCysProGluAspProSerArgGluCysSerSerCysGlyPheH

      1150       1160       1170       1180       1190       1200
ATCAGGCTCAAAGCGGAATTCCAGGCATTATGTGCAGTTTGTGCTACATGCGCCAAACCT
isGlnAlaGlnSerGlyIleProGlyIleMetCysSerLeuCysTyrMetArgGlnThrT

      1210       1220       1230       1240       1250       1260
ACCATTGCATCTATA[GTAAGTACATTCTGTAAAAGAACATCTTGGTGATTTCTAGGTATT
yrHisCysIleTyrS

      1270       1280       1290       1300       1310       1320
GTTTAGGGATTAACTGGGTGGAGTGATCTTAATCCGGCATAACCAAATACATGTTTTCAC

      1330       1340       1350       1360       1370       1380
AG]GTCCAGTTTCTGAAGAGGAAATGTGAGTCATGTTGACTTTGGCGCGC AAGAGGAAATG
   erProValSerGluGluGluMetEnd

      1390       1400       1410       1420       1430       1440
TGAGTCATGTTGACTTTGGCGCGCCCTACGGTGACTTTAAAGCAATTTGAGGATCACTTT

      1450       1460       1470       1480       1490       1500
TTTGTTAGTCGCTATAAAGTAGTCACGGAGTCTTCATGGATCACTTAAGCGTTCTTTTGG
                                      MetAspHisLeuSerValLeuLeuA

      1510       1520       1530       1540       1550       1560
ATTTGAAGCTGCTTCGCTCTATCGTAGCGGGGGCTTCAAATCGCACTGGAGTGTGGAAGA
spLeuLysLeuLeuArgSerIleValAlaGlyAlaSerAsnArgThrGlyValTrpLysA

      1570       1580       1590       1600       1610       1620
GGCGGCTGTGGCTGGGACGCCTGACTCAACTGGTCCATGATACCTGCGTAGAGAACGAGA
rgArgLeuTrpLeuGlyArgLeuThrGlnLeuValHisAspThrCysValGluAsnGluS

      1630       1640       1650       1660       1670       1600
GCATATTTCTCAATTCTCTGCCAGGGAATGAAGCTTTTTTAAGGTTGCTTCGGAGCGGCT
erIlePheLeuAsnSerLeuProGlyAsnGluAlaPheLeuArgLeuLeuArgSerGlyT

      1690       1700       1710       1720       1730       1740
ATTTTGAAGTGTTTGACGTGTTTGTGGTGCCTGAGCTGCATCTGGACACTCCGGGTCGAG
yrPheGluValPheAspValPheValValProGluLeuHisLeuAspThrProGlyArgV
```

FIGURE 1-2

```
      1750       1760       1770       1780       1790       1800
TGGTCGCCGCTCTTGCTCTGCTGGTGTTCATCCTCAACGATTTAGACGCTAATTCTGCTT

alValAlaAlaLeuAlaLeuLeuValPheIleLeuAsnAspLeuAspAlaAsnSerAlaS

      1810       1820       1830       1840       1850       1860
CTTCAGGCTTTGATTCAGGTTTTCTCGTGGACCGTCTCTGCGTGCCGCTATGGCTGAAGG
                                                  MetAlaGluGl
erSerGlyPheAspSerGlyPheLeuValAspArgLeuCysValProLeuTrpLeuLysA

      1870       1880       1890       1900       1910       1920
CCAGGGCGTTCAAGATCACCCAGAGCTCCAGGAGCACTTCGCAGCCTTCCTCGTCGCCCG
yGlnGlyValGlnAspHisProGluLeuGlnGluHisPheAlaAlaPheLeuValAlaAr
laArgAlaPheLysIleThrGlnSerSerArgSerThrSerGlnProSerSerSerProA

      1930       1940       1950       1960       1970       1980
ACAAGACGACCCAGACTACCAGCCAGTAGACGGGGACAGCCCACCCCGGGCTAGCCTGGA
gGlnAspAspProAspTyrGlnProValAspGlyAspSerProProArgAlaSerLeuGl
spLysThrThrGlnThrThrSerGlnEnd

      1990       2000       2010       2020       2030       2040
GGAGGCTGAACAGAGCAGCACTCGTTTCGAGCACATCAGTTACCGAGACGTGGTGGATGA
uGluAlaGluGlnSerSerThrArgPheGluHisIleSerTyrArgAspValValAspAs

      2050       2060       2070       2080       2090       2100
CTTCAATAGATGCCATGATGTTTTTTATGAGAGGTACAGTTTTGAGGACATAAAGAGCTA
pPheAsnArgCysHisAspValPheTyrGluArgTyrSerPheGluAspIleLysSerTy

      2110       2120       2130       2140       2150       2160
CGAGGCTTTGCCTGAGGACAATTTGGAGCAGCTCATAGCTATGCATGCTAAAATCAAGCT
rGluAlaLeuProGluAspAsnLeuGluGlnLeuIleAlaMetHisAlaLysIleLysLe

      2170       2180       2190       2200       2210       2220
GCTGCCCGGTCGGGAGTATGAGTTGACTCAACCTTTGAACATAACATCTTGCGCCTATGT
uLeuProGlyArgGluTyrGluLeuThrGlnProLeuAsnIleThrSerCysAlaTyrVa

      2230       2240       2250       2260       2270       2280
GCTCGGAAATGGGGCTACTATTAGGGTAACAGGGGAAGCCTCCCCGGCTATTAGAGTGGG
lLeuGlyAsnGlyAlaThrIleArgValThrGlyGluAlaSerProAlaIleArgValGl

      2290       2300       2310       2320       2330       2340
GGCCATGGCCGTGGGTCCGTGTGTAACAGGAATGACTGGGGTGACTTTTGTGAATTGTAG
yAlaMetAlaValGlyProCysValThrGlyMetThrGlyValThrPheValAsnCysAr

      2350       2360       2370       2380       2390       2400
GTTTGAGAGAGAGTCAACAATTAGGGGGTCCCTGATACGAGCTTCAACTCACGTGCTGTT
gPheGluArgGluSerThrIleArgGlySerLeuIleArgAlaSerThrHisValLeuPh

      2410       2420       2430       2440       2450       2460
TCATGGCTGTTATTTTATGGGAATTATGGGCACTTGTATTGAGGTGGGGGCGGGAGCTTA
eHisGlyCysTyrPheMetGlyIleMetGlyThrCysIleGluValGlyAlaGlyAlaTy
```

FIGURE 1-3

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```
      2470       2480       2490       2500       2510       2520
CATTCGGGGTTGTGAGTTTGTGGGCTGTTACCGGGGAATCTGTTCTACTTCTAACAGAGA
rIleArgGlyCysGluPheValGlyCysTyrArgGlyIleCysSerThrSerAsnArgAs

      2530       2540       2550       2560       2570       2580
TATTAAGGTGAGGCAGTGCAACTTTGACAAATGCTTACTGGGTATTACTTGTAAGGGGGA
pIleLysValArgGlnCysAsnPheAspLysCysLeuLeuGlyIleThrCysLysGlyAs

      2590       2600       2610       2620       2630       2640
CTATCGTCTTTCGGGAAATGTGTGTTCTGAGACTTTCTGCTTTGCTCATTTAGAGGGAGA
pTyrArgLeuSerGlyAsnValCysSerGluThrPheCysPheAlaHisLeuGluGlyGl

      2650       2660       2670       2680       2690       2700
GGGTTTGGTTAAAAACAACACAGTCAAGTCCCCTAGTCGCTGGACCAGCGAGTCTGGCTT
uGlyLeuValLysAsnAsnThrValLysSerProSerArgTrpThrSerGluSerGlyPh

      2710       2720       2730       2740       2750       2760
TTCCATGATAACTTGTGCAGACGGCAGGGTTACGCCTTTGGGTTCCCTCCACATTGTGGG
eSerMetIleThrCysAlaAspGlyArgValThrProLeuGlySerLeuHisIleValGl


      2770       2780       2790       2800       2810       2820
CAACCGTTGTAGGCGTTGGCCAACCATGCAGGGGAATGTGTTTATCATGTCTAAACTGTA
yAsnArgCysArgArgTrpProThrMetGlnGlyAsnValPheIleMetSerLysLeuTy

      2830       2840       2850       2860       2870       2880
TCTGGGCAACAGAATAGGGACTGTAGCCCTGCCCCAGTGTGCTTTCTACAAGTCCAGCAT
rLeuGlyAsnArgIleGlyThrValAlaLeuProGlnCysAlaPheTyrLysSerSerIl

      2890       2900       2910       2920       2930       2940
TTGTTTGGAGGAGAGGGCGACAAACAAGCTGGTCTTGGCTTGTGCTTTTGAGAATAATGT
eCysLeuGluGluArgAlaThrAsnLysLeuValLeuAlaCysAlaPheGluAsnAsnVa

      2950       2960       2970       2980       2990       3000
ACTGGTGTACAAAGTGCTGAGACGGGAGAGTCCCTCAACCGTGAAAATGTGTGTTTGTGG
lLeuValTyrLysValLeuArgArgGluSerProSerThrValLysMetCysValCysGl

      3010       3020       3030       3040       3050       3060
GACTTCTCATTATGCAAAGCCTTTGACACTGGCAATTATTTCTTCAGATATTCGGGCTAA
yThrSerHisTyrAlaLysProLeuThrLeuAlaIleIleSerSerAspIleArgAlaAs

      3070       3080       3090       3100       3110       3120
TCGATACATGTACACTGTGGACTCAACAGAGTTCACTTCTGACGAGGATTAAAAGTGGGC
nArgTyrMetTyrThrValAspSerThrGluPheThrSerAspGluAspEnd

      3130       3140       3150       3160       3170       3180
GGGGCCAAGAGGGGTATAAATAGGTGGGGAGGTTGAGGGGAGCCGTAGTTTCTGTTTTTC

      3190       3200       3210       3220       3230       3240
CCAGACTGGGGGGGACAACATGGCCGAGGAAGGGCGCATTTATGTGCCTTATGTAACTGC
                  MetAlaGluGluGlyArgIleTyrValProTyrValThrAl
```

FIGURE 1-4

```
      3250       3260       3270       3280       3290       3300
CCGCCTGCCCAAGTGGTCGGGTTCGGTGCAGGATAAGACGGGCTCGAACATGTTGGGGGG
aArgLeuProLysTrpSerGlySerValGlnAspLysThrGlySerAsnMetLeuGlyGl
      3310       3320       3330       3340       3350       3360
TGTGGTACTCCCTCCTAATTCACAGGCGCACCGGACGGAGACCGTGGGCACTGAGGCCAC
yValValLeuProProAsnSerGlnAlaHisArgThrGluThrValGlyThrGluAlaTh

      3370       3380       3390       3400       3410       3420
CAGAGACAACCTGCACGCCGAGGGAGCGCGTCGTCCTGAGGATCAGACGCCCTACATGAT
rArgAspAsnLeuHisAlaGluGlyAlaArgArgProGluAspGlnThrProTyrMetIl

      3430       3440       3450       3460       3470       3480
CTTGGTGGAGGACTCTCTGGGAGGTTTGAAGAGGCGAATGGACTTGCTGGAAGAATCTAA
eLeuValGluAspSerLeuGlyGlyLeuLysArgArgMetAspLeuLeuGluGluSerAs

      3490       3500       3510       3520       3530       3540
TCAGCAGCTGCTGGCAACTCTCAACCGTCTCCGTACAGGACTCGCTGCCTATGTGCAGGC
nGlnGlnLeuLeuAlaThrLeuAsnArgLeuArgThrGlyLeuAlaAlaTyrValGlnAl

      3550       3560       3570       3580       3590       3600
TAACCTTGTGGGCGGCCAAGTTAACCCCTTTGTTTAAATAAAAATACACTCATACAGTTT
aAsnLeuValGlyGlyGlnValAsnProPheValEnd

      3610       3620       3630       3640       3650       3660
ATTATGCTGTCAATAAAATTCTTTATTTTTCCTGTGATAATACCGTGTCCAGCGTGCTCT

      3670       3680       3690       3700       3710       3720
GTCAATAAGGGTCCTATGCATCCTGAGAAGGGCCTCATATACCCATGGCATGAATATTAA

      3730       3740       3750       3760       3770       3780
GATACATGGGCATAAGGCCCTCAGAAGGGTTGAGGTAGAGCCACTGCAGACTTTCGTGGG

      3790       3800       3810       3820       3830       3840
GAGGTAAGGTGTTGTAAATAATCCAGTCATACTGACTGTGCTGGGCGTGGAAGGAAAAGA

      3850       3860       3870       3880       3890       3900
TGTCTTTTAGAAGAAGGGTGATTGGCAAAGGGAGGCTCTTAGTGTAGGTATTGATAAATC

      3910       3920       3930       3940       3950       3960
TGTTCAGTTGGGAGGGATGCATTCGGGGGCTAATAAGGTGGAGTTTAGCCTGAATCTTAA

      3970       3980       3990       4000       4010       4020
GGTTGGCAATGTTGCCCCCTAGGTCTTTGCGAGGATTCATGTTGTGCAGTACCACAAAAA

      4030       4040       4050       4060
CAGAGTAGCCTGTGCATTTGGGGAATTTATCATGAAGCTT
```

FIGURE 1-5

A.

ACTIVATION REGION

```
Ad5     140 -                                                  153
        GluGluPheValLeuAspTyr   ValGlu          HisProGlyHisGly
         |  |                   :    :  :          |     :
        GluGluValThrSerHisPhePheLeuAspCysProGluAspProSerArgGlu
BAV3    155                                                    172
```

METAL BINDING REGION

```
Ad5   154                                                      174
      CysArgSerCysHisTyrHisArgArgAsnThrGlyAspProAspIleMetCysSerLeuCys
       |     |  |     :  |        :  :  |     |     |  |  |  |  |  |
      CysSerSerCysGlyPheHisGlnAlaGlnSerGlyIleProGlyIleMetCysSerLeuCys
BAV3  173                                                      193
```

PROMOTER BINDING REGION

```
Ad5    175                                        189
       TyrMetArgThrCys   GlyMetPheValTyrSerProValSerGluProGluProGlu
        |  |  |              :  |  |  |  |  |  |     |
       TyrMetArgGlnThrTyrHisCys   IleTyrSerProValSerGluGluGluMetEnd
BAV3   194                                        208
```

B.

Rb BINDING SEQUENCE

```
Ad5     120                                 132
        IleAspLeuThrCysHisGluAlaGlyPheProProSer
         :  |  |     |  |  |              |  |  |
        ValAspLeuGluCysHisGluVal   LeuProProSer
BAV3    26                                  37
```

FIGURE 2

A.

```
Ad5     82  -                                                    100
        LeuAspPheSerThrProGlyArgAlaAlaAlaAlaValAlaPheLeuSerPheIle
         |  |        |  |  |  |        |  |     |     |     |  |
        LeuAsp      ThrProGlyArgValValAlaAlaLeuAlaLeuLeuValPheIle
BAV3    83                                                    99
```

B.

```
Ad5     20                26
        GlnSerSerAsnSerThrSer
         |  |  |     |  |  |
        GlnSerSerArgSerThrSer
BAV3    136               142
```

Substitute Sheet (Rule 26)

FIGURE 3

```
Ad5  150  GlnLysTyrSerIleGluGlnLeuThrThrTyrTrpLeuGlnProGlyAspAspPheGlu
BAV3  74  GluArgTyrLysPheGluAspIleLysSerTyrGluAlaLeuProGluAspAsnLeuGlu

170       GluAlaIleArgValTyrAlaLysValAlaLeuArgProAspCysLysTyrLysIleSer
 94    -  GlnLeuIleAlaMetHisAlaLysIleLysLeuLeuProGlyArgGluTyrGluLeuThr

190       LysLeuValAsnIleArgAsnCysCysTyrIleSerGlyAsnGlyAlaGluValGluIle
114       GlnProLeuAsnIleThrSerCysAlaTyrValLeuGlyAsnGlyAlaThrIleArgVal

210       AspThrGluAspArgValAlaPheArgCysSerMetIleAsnMetTrpProGlyValLeu
134       ThrGlyGluAlaSerProAlaIleArgValGlyAlaMetAlaValGlyProCysValThr

230       GlyMetAspGlyValValIleMetAsnValArgPheThr  GlyProAsnPheSerGly
154       GlyMetThrGlyValThrPheValAsnCysArgPheGluArgGluSerThrIleArgGly

249       ThrValPheLeuAlaAsnThrAsnLeuIleLeuHisGlyValSerPheTyr  GlyPhe
174       SerLeuIleArgAlaSerThrHisValLeuPheHisGlyCys  TyrPheMetGlyIle

268       AsnAsnThrCysValGluAlaTrpThrAspValArgValArgGlyCysAlaPheTyrCys
193       MetGlyThrCysIleGluValGlyAlaGlyAlaTyrIleArgGlyCysGluPheValGly

288       CysTrpLysGlyValValCysArgProLysSerArgAla  SerIleLysLysCysLeu
213       CysTyrArgGlyIle  CysSerThrSerAsnArgAspIleLysValArgGlnCysAsn

307       PheGluArgCysThrLeuGlyIleLeuSerGluGlyAsnSerArgValArgHisAsnVal
232       PheAspLysCysLeuLeuGlyIleThrCysLysGlyAspTyrArgLeuSerGlyAsnVal

327       AlaSerAspCysGlyCysPheMetLeuValLysSerValAlaValIleLysHisAsnMet
252       CysSerGluThrPheCysPheAlaHisLeuGluGlyGluGlyLeuValLysAsnAsnThr

347       Val  CysGlyAsn  CysGluAspArgAlaSerGlnMetLeuThrCysSerAsp
272       ValLysSerProSerArgTrpThrSerGluSerGlyPheSerMetIleThrCysAlaAsp

364       GlyAsnCysHisLeuLeuLysThrIleHisVal  AlaSerHisSerArgLysAlaTrp
292       GlyArgValThrProLeuGlySerLeuHisIleValGlyAsnArgCysArgArg  Trp

383       ProValPheGluHisAsnIleLeuThrArgCysSerLeuHisLeuGlyAsnArgArgGly
311       ProThrMetGlnGlyAsnValPheIleMetSerLysLeuTyrLeuGlyAsnArgIleGly

403         ValPheLeuProTyrGlnCysAsnLeuSerHisThrLysIleLeuLeuGluProGlu
331       ThrValAlaLeuPro  GlnCysAlaPheTyrLysSerSerIleCysLeuGluGluArg

422       SerMetSerLysValAsnLeuAsnGlyValPheAspMetThrMetLysIleTrpLysVal
350       AlaThrAsnLysLeuValLeuAlaCysAlaPheGluAsnAsnValLeuValTyrLysVal

442       LeuArgTyrAspGluThrArgThrArgCysArgProCysGluCysGlyGlyLysHisIle
370       LeuArgArgGluSerProSerThr  ValLysMetCysValCysGlyThrSerHisTyr

462       ArgAsnGlnProValMetLeuAspVal  ThrGluGluLeuArgProAspHisLeuVal
389         AlaLysProLeuThrLeuAlaIleIleSerSerAspIleArgAlaAsnArgTyrMet

481       LeuAlaCysThrArgAlaGluPheGlySerSerAspGluAspThrAspEnd
408       TyrThrValAspSerThrGluPhe  ThrSerAspGluAspEnd
```

FIGURE 4

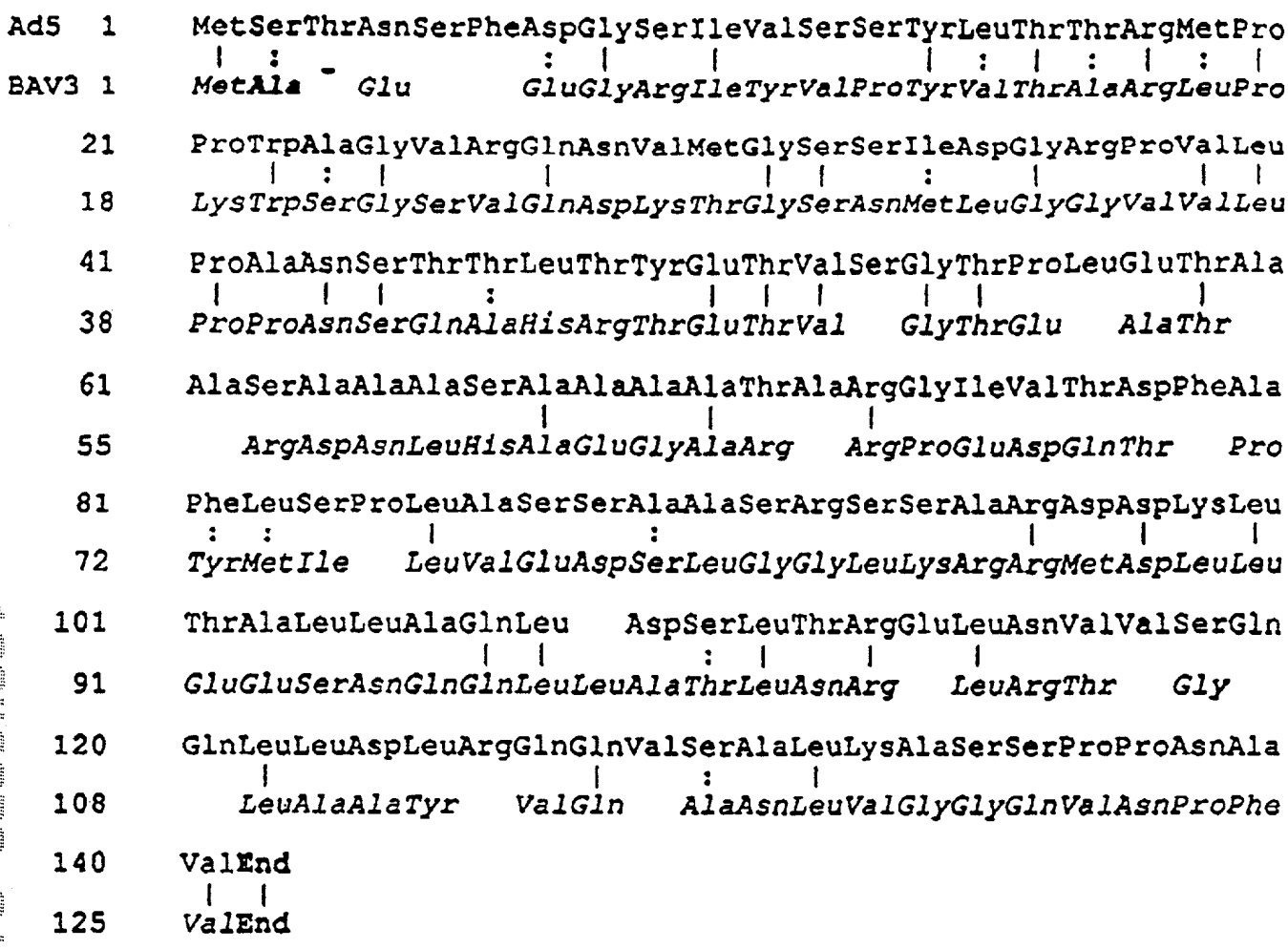
Ad5 1 MetSerThrAsnSerPheAspGlySerIleValSerSerTyrLeuThrThrArgMetPro
BAV3 1 MetAla Glu GluGlyArgIleTyrValProTyrValThrAlaArgLeuPro
21 ProTrpAlaGlyValArgGlnAsnValMetGlySerSerIleAspGlyArgProValLeu
18 LysTrpSerGlySerValGlnAspLysThrGlySerAsnMetLeuGlyGlyValValLeu
41 ProAlaAsnSerThrThrLeuThrTyrGluThrValSerGlyThrProLeuGluThrAla
38 ProProAsnSerGlnAlaHisArgThrGluThrVal GlyThrGlu AlaThr
61 AlaSerAlaAlaAlaSerAlaAlaAlaAlaThrAlaArgGlyIleValThrAspPheAla
55 ArgAspAsnLeuHisAlaGluGlyAlaArg ArgProGluAspGlnThr Pro
81 PheLeuSerProLeuAlaSerSerAlaAlaSerArgSerSerAlaArgAspAspLysLeu
72 TyrMetIle LeuValGluAspSerLeuGlyGlyLeuLysArgArgMetAspLeuLeu
101 ThrAlaLeuLeuAlaGlnLeu AspSerLeuThrArgGluLeuAsnValValSerGln
91 GluGluSerAsnGlnGlnLeuLeuAlaThrLeuAsnArg LeuArgThr Gly
120 GlnLeuLeuAspLeuArgGlnGlnValSerAlaLeuLysAlaSerSerProProAsnAla
108 LeuAlaAlaTyr ValGln AlaAsnLeuValGlyGlyGlnValAsnProPhe
140 ValEnd
125 ValEnd

FIGURE 5

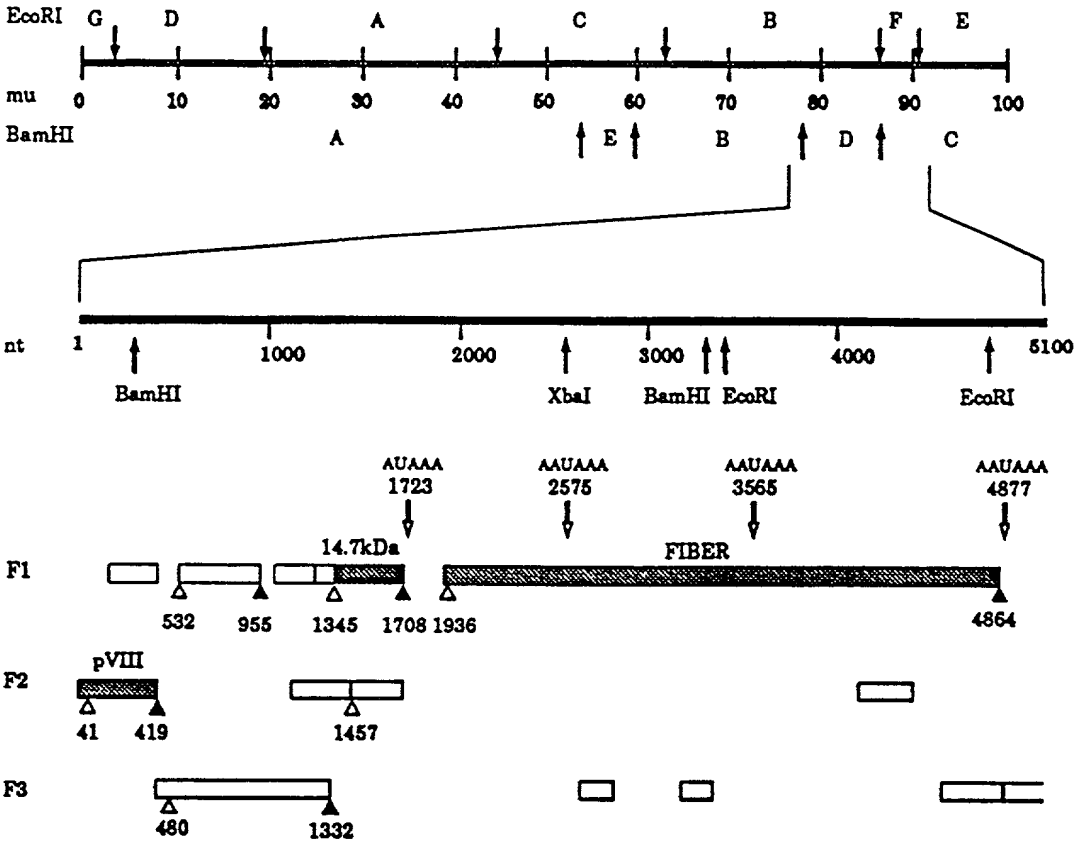
EcoRI
G
D
A
C
B
F
E
mu
0
10
20
30
40
50
60
70
80
90
100
BamHI
A
E
B
D
C
nt
1
1000
2000
3000
4000
5100
BamHI
XbaI
BamHI
EcoRI
EcoRI
AUAAA
1723
AAUAAA
2575
AAUAAA
3565
AAUAAA
4877
14.7kDa
FIBER
F1
532
955
1345
1708
1936
4864
pVIII
F2
41
419
1457
F3
480
1332

FIGURE 6

```
                10                  20                  30                  40                  50
    C CTC ATC AAA CAA CCC GTG GTG GGC ACC ACC CAC GTG GAA ATG CCT CGC AAC
ORF 1  Leu Ile Lys Gln Pro Val Val Gly Thr Thr His Val Glu Met Pro Arg Asn

          60                  70                  80                  90                 100
    GAA GTC CTA GAA CAA CAT CTG ACC TCA CAT GGC GCT CAA ATC GCG GGC GGA
    Glu Val Leu Glu Gln His Leu Thr Ser His Gly Ala Gln Ile Ala Gly Gly

        110                 120                 130                 140                 150
    GGC GCT GCG GGC GAT TAC TTT AAA AGC CCC ACT TCA GCT CGA ACC CTT ATC
    Gly Ala Ala Gly Asp Tyr Phe Lys Ser Pro Thr Ser Ala Arg Thr Leu Ile

      160                 170                 180                 190                 200
    CCG CTC ACC GCC TCC TGC TTA AGA CCA GAT GGA GTC TTT CAA CTA GGA GGA
    Pro Leu Thr Ala Ser Cys Leu Arg Pro Asp Gly Val Phe Gln Leu Gly Gly

    210                 220                 230                 240                 250
    GGC TCG CGT TCA TCT TTC AAC CCC CTG CAA ACA GAT TTT GCC TTC CAC GCC
    Gly Ser Arg Ser Ser Phe Asn Pro Leu Gln Thr Asp Phe Ala Phe His Ala

    260                 270                 280                 290                 300
    CTG CCC TCC AGA CCG CGC CAC GGG GGC ATA GGA TCC AGG CAG TTT GTA GAG
    Leu Pro Ser Arg Pro Arg His Gly Gly Ile Gly Ser Arg Gln Phe Val Glu

    310                 320                 330                 340                 350
    GAA TTT GTG CCC GCC GTC TAC CTC AAC CCC TAC TCG GGA CCG CCG GAC TCT
    Glu Phe Val Pro Ala Val Tyr Leu Asn Pro Tyr Ser Gly Pro Pro Asp Ser

  360                 370                 380                 390                 400
    TAT CCG GAC CAG TTT ATA CGC CAC TAC AAC GTG TAC AGC AAC TCT GTG AGC
    Tyr Pro Asp Gln Phe Ile Arg His Tyr Asn Val Tyr Ser Asn Ser Val Ser
                                                                ORF 2  Ala

410                 420                 430                 440                 450                 460
    GGT TAT AGC T GAG ATT GTA AGA CTC TCC TAT CTG TCT CTG TGC TGC TTT TCC
    Gly Tyr Ser
     Val Ile Ala  Glu Ile Val Arg Leu Ser Tyr Leu Ser Leu Cys Cys Phe Ser

          470                 480                 490                 500                 510
    GCT TCA AGC CCC ACA AGC ATG AAG GGG TTT CTG CTC ATC TTC AGC CTG CTT
    Ala Ser Ser Pro Thr Ser Met Lys Gly Phe Leu Leu Ile Phe Ser Leu Leu

        520                 530                 540                 550                 560
    GTG CAT TGT CCC CTA ATT CAT GTT GGG ACC ATT AGC TTC TAT GCT GCA AGG
                    ORF 3  Phe Met Leu Gly Pro Leu Ala Ser Met Leu Gln Gly
    Val His Cys Pro Leu Ile His Val Gly Thr Ile Ser Phe Tyr Ala Ala Arg

          570                 580                 590                 600                 610
     CCC GGG TCT GAG CCT AAC GCG ACT TAT GTT TGT GAC TAT GGA AGC GAG TCA
      Pro Gly Leu Ser Leu Thr Arg Leu Met Phe Val Thr Met Glu Ala Ser Gln
     Pro Gly Ser Glu Pro Asn Ala Thr Tyr Val Cys Asp Tyr Gly Ser Glu Ser

        620                 630                 640                 650                 660
    GAT TAC AAC CCC ACC ACG GTT CTG TGG TTG GCT CGA GAG ACC GAT GGC TCC
     Ile Thr Thr Pro Pro Arg Phe Cys Gly Trp Leu Glu Arg Pro Met Ala Pro
    Asp Tyr Asn Pro Thr Thr Val Leu Trp Leu Ala Arg Glu Thr Asp Gly Ser
```

FIGURE 7-1

```
   670          68           690          70           710
TGG ATC TCT GTT CT  TTC CGT CAC AAC GGC TCC TCA ACT GCA GCC CCC GGG
 Gly Ser Leu Phe Phe Ser Val Thr Thr Ala Pro Gln Leu Gln Pro Pro Gly
Trp Ile Ser Val Leu Phe Arg His Asn Gly Ser Ser Thr Ala Ala Pro Gly

  720          730          740          750          760
GTC GTC GCG CAC TTT ACT GAC CAC AAC AGC AGC ATT GTG GTG CCC CAG TAT
 Ser Ser Arg Thr Leu Leu Thr Thr Thr Ala Ala Leu Trp Cys Pro Ser Ile
Val Val Ala His Phe Thr Asp His Asn Ser Ser Ile Val Val Pro Gln Tyr

770          780          790          800          810
TAC CTC CTC AAC AAC TCA CTC TCT AAG CTC TGC TGC TCA TAC CGG CAC AAC
 Thr Ser Ser Thr Thr His Ser Leu Ser Ser Ala Ala His Thr Gly Thr Thr
Tyr Leu Leu Asn Asn Ser Leu Ser Lys Leu Cys Cys Ser Tyr Arg His Asn

820          830          840          850          860
GAG CGT TCT CAG TTT ACC TGC AAA CAA GCT GAC GTC CCT ACC TGT CAC GAG
 Ser Val Leu Ser Leu Pro Ala Asn Lys Leu Thr Ser Leu Pro Val Thr Ser
Glu Arg Ser Gln Phe Thr Cys Lys Gln Ala Asp Val Pro Thr Cys His Glu

870          880          890          900          910          920
CCC GGC AAG CCG CTC ACC CTC CGC GTC TCC CCC GCG CTG GGA ACT GCC CAC
 Pro Ala Ser Arg Ser Pro Ser Ala Ser Pro Pro Arg Trp Glu Leu Pro Thr
Pro Gly Lys Pro Leu Thr Leu Arg Val Ser Pro Ala Leu Gly Thr Ala His

          930          940          950          960          970
CAA GCA GTC ACT TGG TTT TTT CAA AAT GTA CCC ATA GCT ACT GTT TAC CGA
 Lys Gln Ser Leu Gly Phe Phe Lys Met Tyr Pro
Gln Ala Val Thr Trp Phe Phe Gln Asn Val Pro Ile Ala Thr Val Tyr Arg

        980          990          1000         1010         1020
CCT TGG GGC AAT GTA ACT TGG TTT TGT CCT CCC TTC ATG TGT ACC TTT AAT
Pro Trp Gly Asn Val Thr Trp Phe Cys Pro Pro Phe Met Cys Thr Phe Asn

      1030         1040         1050         1060         1070
GTC AGC CTG AAC TCC CTA CTT ATT TAC AAC TTT TCT GAC AAA ACC GGG GGG
Val Ser Leu Asn Ser Leu Leu Ile Tyr Asn Phe Ser Asp Lys Thr Gly Gly

     1080         1090         1100         1110         1120
CAA TAC ACA GCT CTC ATG CAC TCC GGA CCT GCT TCC CTC TTT CAG CTC TTT
Gln Tyr Thr Ala Leu Met His Ser Gly Pro Ala Ser Leu Phe Gln Leu Phe

   1130         1140         1150         1160         1170
AAG CCA ACG ACT TGT GTC ACC AAG GTG GAG GAC CCG CCG TAT GCC AAC GAC
Lys Pro Thr Thr Cys Val Thr Lys Val Glu Asp Pro Pro Tyr Ala Asn Asp

  1180         1190         1200         1210         1220
CCG GCC TCG CCT GTG TGG CGC CCA CTG CTT TTT GCC TTC GTC CTC TGC ACC
Pro Ala Ser Pro Val Trp Arg Pro Leu Leu Phe Ala Phe Val Leu Cys Thr

 1230         1240         1250         1260         1270
GGC TGC GCG GTG TTG TTA ACC GCC TTC GGT CCA TCG ATT CTA TCC GGT ACC
                    ORF 4  Pro Pro Ser Val His Arg Phe Tyr Pro Val Pro
Gly Cys Ala Val Leu Leu Thr Ala Phe Gly Pro Ser Ile Leu Ser Gly Thr
```

FIGURE 7-2

```
1280          1290          1300          1310          1320
CGA AAG CTT ATC TC  GCC CGC TTT TGG AGT CCC G.  CCC TAT ACC ACC CTC
 Glu Ser Leu Ser Gln Pro Ala Phe Gly Val Pro Ser Pro Ile Pro Pro Ser
Arg Lys Leu Ile Ser Ala Arg Phe Trp Ser Pro Glu Pro Tyr Thr Thr Leu

1330          1340          1350          1360          1370          1380
CAC T AAC AGT CCC CCC ATG GAG CCA GAC GGA GTT CAT GCC GAG CAG CAG TTT
 Thr  Asn Ser Pro Pro Met Glu Pro Asp Gly Val His Ala Glu Gln Gln Phe
His

          1390          1400          1410          1420          1430
ATC CTC AAT CAG ATT TCC TGC GCC AAC ACT GCC CTC CAG CGT CAA AGG GAG
Ile Leu Asn Gln Ile Ser Cys Ala Asn Thr Ala Leu Gln Arg Gln Arg Glu

       1440          1450          1460          1470          1480
GAA CTA GCT TCC CTT GTC ATG TTG CAT GCC TGT AAG CGT GGC CTC TTT TGT
Glu Leu Ala Ser Leu Val Met Leu His Ala Cys Lys Arg Gly Leu Phe Cys
  ORF 5  Leu Pro Leu Ser Cys Cys Met Pro Val Ser Val Ala Ser Phe Val

      1490          1500          1510          1520          1530
CCA GTC AAA ACT TAC AAG CTC AGC CTC AAC GCC TCG GCC AGC GAG CAC AGC
Pro Val Lys Thr Tyr Lys Leu Ser Leu Asn Ala Ser Ala Ser Glu His Ser
 Gln Ser Lys Leu Thr Ser Ser Ala Ser Thr Pro Arg Pro Ala Ser Thr Ala

     1540          1550          1560          1570          1580
CTG CAC TTT GAA AAA AGT CCC TCC CGA TTC ACC CTG GTC AAC ACT CAC GCC
Leu His Phe Glu Lys Ser Pro Ser Arg Phe Thr Leu Val Asn Thr His Ala
 Cys Thr Leu Lys Lys Val Pro Pro Asp Ser Pro Trp Ser Thr Leu Thr Pro

   1590          1600          1610          1620          1630
GGA GCT TCT GTG CGA GTG GCC CTA CAC CAC CAG GGA GCT TCC GGC AGC ATC
Gly Ala Ser Val Arg Val Ala Leu His His Gln Gly Ala Ser Gly Ser Ile
 Glu Leu Leu Cys Glu Trp Pro Tyr Thr Thr Arg Glu Leu Pro Ala Ala Ser

  1640          1650          1660          1670          1680
CGC TGT TCC TGT TCC CAC GCC GAG TGC CTC CCC GTC CTC CTC AAG ACC CTC
Arg Cys Ser Cys Ser His Ala Glu Cys Leu Pro Val Leu Leu Lys Thr Leu
 Ala Val Pro Val Pro Thr Pro Ser Ala Ser Pro Ser Ser Ser Arg Pro Ser

 1690          1700          1710       1720       1730       1740
TGT GCC TTT AAC TTT TTA GAT TAG CTGAAAGCAA ATATAAAATG GTGTGCTTAC
Cys Ala Phe Asn Phe Leu Asp
 Val Pro Leu Thr Phe

      1750       1760          1770          1780          1790
CGTAATTCTG TTTTGACTTG TGTGCTTGA TTT CTC CCC CTG CGC CGT AAT CCA GTG

 1800          1810          1820          1830          1840
CCC CTC TTC AAA ACT CTC GTA CCC TAT GCG ATT CGC ATA GGC ATA TTT TCT

1850          1860          1870          1880          1890
AAA AGC TCT GAA GTC AAC ATC ACT CTC AAA CAC TTC TCC GTT GTA GGT TAC

1900          1910          1920          1930          1940          1950
TTT CAT CTA CAG ATA AAG TCA TCC ACC GGT T AAC ATC ATG AAG AGA AGT GTG
                ORF 6  Ser His Pro Pro Val  Asn Ile Met Lys Arg Ser Val
```

FIGURE 7-3

```
          1960         1970         1980         1990         2000
CCC CAG GAC TTT AA. CTT GTG TAT CCG TAC AAG GC. AAG AGG CCC AAC ATC
Pro Gln Asp Phe Asn Leu Val Tyr Pro Tyr Lys Ala Lys Arg Pro Asn Ile

       2010         2020         2030         2040         2050
ATG CCG CCC TTT TTT GAC CGC AAT GGC TTT GTT GAA AAC CAA GAA GCC ACG
Met Pro Pro Phe Phe Asp Arg Asn Gly Phe Val Glu Asn Gln Glu Ala Thr

       2060         2070         2080         2090         2100
CTA GCC ATG CTT GTG GAA AAG CCG CTC ACG TTC GAC AAG GAA GGT GCG CTG
Leu Ala Met Leu Val Glu Lys Pro Leu Thr Phe Asp Lys Glu Gly Ala Leu

       2110         2120         2130         2140         2150
ACC CTG GGC GTC GGA CGC GGC ATC CGC ATT AAC CCC GCG GGG CTT CTG GAG
Thr Leu Gly Val Gly Arg Gly Ile Arg Ile Asn Pro Ala Gly Leu Leu Glu

       2160         2170         2180         2190         2200
ACA AAC GAC CTC GCG TCC GCT GTC TTC CCA CCG CTG GCC TCC GAT GAG GCC
Thr Asn Asp Leu Ala Ser Ala Val Phe Pro Pro Leu Ala Ser Asp Glu Ala

       2210         2220         2230         2240         2250
GGC AAC GTC ACG CTC AAC ATG TCT GAC GGG CTA TAT ACT AAG GAC AAC AAG
Gly Asn Val Thr Leu Asn Met Ser Asp Gly Leu Tyr Thr Lys Asp Asn Lys

       2260         2270         2280         2290         2300
CTA GCT GTC AAA GTA GGT CCC GGG CTG TCC CTC GAC TCC AAT AAT GCT CTC
Leu Ala Val Lys Val Gly Pro Gly Leu Ser Leu Asp Ser Asn Asn Ala Leu

       2310         2320         2330         2340         2350
CAG GTC CAC ACA GGC GAC GGG CTC ACG GTA ACC GAT GAC AAG GTG TCT CTA
Gln Val His Thr Gly Asp Gly Leu Thr Val Thr Asp Asp Lys Val Ser Leu

       2360         2370         2380         2390         2400
AAT ACC CAA GCT CCC CTC TCG ACC ACC AGC GCG GGC CTC TCC CTA CTT CTG
Asn Thr Gln Ala Pro Leu Ser Thr Thr Ser Ala Gly Leu Ser Leu Leu Leu

       2410         2420         2430         2440         2450         2460
GGT CCC AGC CTC CAC TTA GGT GAG GAG GAA CGA CTA ACA GTA AAC ACC GGA
Gly Pro Ser Leu His Leu Gly Glu Glu Glu Arg Leu Thr Val Asn Thr Gly

          2470         2480         2490         2500         2510
GCG GGC CTC CAA ATT AGC AAT AAC GCT CTG GCC GTA AAA GTA GGT TCA GGT
Ala Gly Leu Gln Ile Ser Asn Asn Ala Leu Ala Val Lys Val Gly Ser Gly

       2520         2530         2540         2550         2560
ATC ACC GTA GAT GCT CAA AAC CAG CTC GCT GCA TCC CTG GGG GAC GGT CTA
Ile Thr Val Asp Ala Gln Asn Gln Leu Ala Ala Ser Leu Gly Asp Gly Leu

       2570         2580         2590         2600         2610
GAA AGC AGA GAT AAT AAA ACT GTC GTT AAG GCT GGG CCC GGA CTT ACA ATA
Glu Ser Arg Asp Asn Lys Thr Val Val Lys Ala Gly Pro Gly Leu Thr Ile

       2620         2630         2640         2650         2660
ACT AAT CAA GCT CTT ACT GTT GCT ACC GGG AAC GGC CTT CAG GTC AAC CCG
Thr Asn Gln Ala Leu Thr Val Ala Thr Gly Asn Gly Leu Gln Val Asn Pro
```

FIGURE 7-4

```
   2670          2680          2690          2700          2710
GAA GGG CAA CTG CAG CTA AAC ATT ACT GCC GGT CAG GGC CTC AAC TTT GCA
Glu Gly Gln Leu Gln Leu Asn Ile Thr Ala Gly Gln Gly Leu Asn Phe Ala

   2720          2730          2740          2750          2760
AAC AAC AGC CTC GCC GTG GAG CTG GGC TCG GGC CTG CAT TTT CCC CCT GGC
Asn Asn Ser Leu Ala Val Glu Leu Gly Ser Gly Leu His Phe Pro Pro Gly

   2770          2780          2790          2800          2810
CAA AAC CAA GTA AGC CTT TAT CCC GGA GAT GGA ATA GAC ATC CGA GAT AAT
Gln Asn Gln Val Ser Leu Tyr Pro Gly Asp Gly Ile Asp Ile Arg Asp Asn

   2820          2830          2840          2850          2860
AGG GTG ACT GTG CCC GCT GGG CCA GGC CTG AGA ATG CTC AAC CAC CAA CTT
Arg Val Thr Val Pro Ala Gly Pro Gly Leu Arg Met Leu Asn His Gln Leu

   2870          2880          2890          2900          2910
GCC GTA GCT TCC GGA GAC GGT TTA GAA GTC CAC AGC GAC ACC CTC CGG TTA
Ala Val Ala Ser Gly Asp Gly Leu Glu Val His Ser Asp Thr Leu Arg Leu

   2920          2930          2940          2950          2960          2970
AAG CTC TCC CAC GGC CTG ACA TTT GAA AAT GGC GCC GTA CGA GCA AAA CTA
Lys Leu Ser His Gly Leu Thr Phe Glu Asn Gly Ala Val Arg Ala Lys Leu

            2980          2990          3000          3010          3020
GGA CCA GGA CTT GGC ACA GAC GAC TCT GGT CGG TCC GTG GTT CGC ACA GGT
Gly Pro Gly Leu Gly Thr Asp Asp Ser Gly Arg Ser Val Val Arg Thr Gly

         3030          3040          3050          3060          3070
CGA GGA CTT AGA GTT GCA AAC GGC CAA GTC CAG ATC TTC AGC GGA AGA GGC
Arg Gly Leu Arg Val Ala Asn Gly Gln Val Gln Ile Phe Ser Gly Arg Gly

         3080          3090          3100          3110          3120
ACC GCC ATC GGC ACT GAT AGC AGC CTC ACT CTC AAC ATC CGG GCG CCC CTA
Thr Ala Ile Gly Thr Asp Ser Ser Leu Thr Leu Asn Ile Arg Ala Pro Leu

      3130          3140          3150          3160          3170
CAA TTT TCT GGA CCC GCC TTG ACT GCT AGT TTG CAA GGC AGT GGT CCG ATT
Gln Phe Ser Gly Pro Ala Leu Thr Ala Ser Leu Gln Gly Ser Gly Pro Ile

   3180          3190          3200          3210          3220
ACT TAC AAC AGC AAC AAT GGC ACT TTC GGT CTC TCT ATA GGC CCC GGA ATG
Thr Tyr Asn Ser Asn Asn Gly Thr Phe Gly Leu Ser Ile Gly Pro Gly Met

   3230          3240          3250          3260          3270
TGG GTA GAC CAA AAC AGA CTT CAG GTA AAC CCA GGC GCT GGT TTA GTC TTC
Trp Val Asp Gln Asn Arg Leu Gln Val Asn Pro Gly Ala Gly Leu Val Phe

   3280          3290          3300          3310          3320
CAA GGA AAC AAC CTT GTC CCA AAC CTT GCG GAT CCG CTG GCT ATT TCC GAC
Gln Gly Asn Asn Leu Val Pro Asn Leu Ala Asp Pro Leu Ala Ile Ser Asp

   3330          3340          3350          3360          3370
AGC AAA ATT AGT CTC AGT CTC GGT CCC GGC CTG ACC CAA GCT TCC AAC GCC
Ser Lys Ile Ser Leu Ser Leu Gly Pro Gly Leu Thr Gln Ala Ser Asn Ala
```

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FIGURE 7-5

```
3380          3390          3400          3410          3420
  CTG ACT TTA AGT TTA GGA AAC GGG CTT GAA TTC TCC AAT CAA GCC GTT GCT
  Leu Thr Leu Ser Leu Gly Asn Gly Leu Glu Phe Ser Asn Gln Ala Val Ala

3430          3440          3450          3460          3470          3480
  ATA AAA GCG GGC CGG GGC TTA CGC TTT GAG TCT TCC TCA CAA GCT TTA GAG
  Ile Lys Ala Gly Arg Gly Leu Arg Phe Glu Ser Ser Ser Gln Ala Leu Glu

          3490          3500          3510          3520          3530
  AGC AGC CTC ACA GTC GGA AAT GGC TTA ACG CTT ACC GAT ACT GTG ATC CGC
  Ser Ser Leu Thr Val Gly Asn Gly Leu Thr Leu Thr Asp Thr Val Ile Arg

        3540          3550          3560          3570          3580
  CCC AAC CTA GGG GAC GGC CTA GAG GTC AGA GAC AAT AAA ATC ATT GTT AAG
  Pro Asn Leu Gly Asp Gly Leu Glu Val Arg Asp Asn Lys Ile Ile Val Lys

        3590          3600          3610          3620          3630
  CTG GGC GCG AAT CTT CGT TTT GAA AAC GGA GCC GTA ACC GCC GGC ACC GTT
  Leu Gly Ala Asn Leu Arg Phe Glu Asn Gly Ala Val Thr Ala Gly Thr Val

      3640          3650          3660          3670          3680
  AAC CCT TCT GCG CCC GAG GCA CCA CCA ACT CTC ACT GCA GAA CCA CCC CTC
  Asn Pro Ser Ala Pro Glu Ala Pro Pro Thr Leu Thr Ala Glu Pro Pro Leu

    3690          3700          3710          3720          3730
  CGA GCC TCC AAC TCC CAT CTT CAA CTG TCC CTA TCG GAG GGC TTG GTT GTG
  Arg Ala Ser Asn Ser His Leu Gln Leu Ser Leu Ser Glu Gly Leu Val Val

   3740          3750          3760          3770          3780
  CAT AAC AAC GCC CTT GCT CTC CAA CTG GGA GAC GGC ATG GAA GTA AAT CAG
  His Asn Asn Ala Leu Ala Leu Gln Leu Gly Asp Gly Met Glu Val Asn Gln

  3790          3800          3810          3820          3830
  CAC GGA CTT ACT TTA AGA GTA GGC TCG GGT TTG CAA ATG CGT GAC GGC ATT
  His Gly Leu Thr Leu Arg Val Gly Ser Gly Leu Gln Met Arg Asp Gly Ile

 3840          3850          3860          3870          3880
  TTA ACA GTT ACA CCC AGC GGC ACT CCT ATT GAG CCC AGA CTG ACT GCC CCA
  Leu Thr Val Thr Pro Ser Gly Thr Pro Ile Glu Pro Arg Leu Thr Ala Pro

 3890          3900          3910          3920          3930
  CTG ACT CAG ACA GAG AAT GGA ATC GGG CTC GCT CTC GGC GCC GGC TTG GAA
  Leu Thr Gln Thr Glu Asn Gly Ile Gly Leu Ala Leu Gly Ala Gly Leu Glu

3940          3950          3960          3970          3980          3990
  TTA GAC GAG AGC GCG CTC CAA GTA AAA GTT GGG CCC GGC ATG CGC CTG AAC
  Leu Asp Glu Ser Ala Leu Gln Val Lys Val Gly Pro Gly Met Arg Leu Asn

          4000          4010          4020          4030          4040
  CCT GTA GAA AAG TAT GTA ACC CTG CTC CTG GGT CCT GGC CTT AGT TTT GGG
  Pro Val Glu Lys Tyr Val Thr Leu Leu Leu Gly Pro Gly Leu Ser Phe Gly

        4050          4060          4070          4080          4090
  CAG CCG GCC AAC AGG ACA AAT TAT GAT GTG CGC GTT TCT GTG GAG CCC CCC
  Gln Pro Ala Asn Arg Thr Asn Tyr Asp Val Arg Val Ser Val Glu Pro Pro
```

FIGURE 7-6

```
      4100        4110        4120        4130        4140
ATG GTT TTC GGA CA  CGT GGT CAG CTC ACA TTT TTA GTG GGT CAC GGA CTA
Met Val Phe Gly Gln Arg Gly Gln Leu Thr Phe Leu Val Gly His Gly Leu

      4150        4160        4170        4180        4190
CAC ATT CAA AAT TCC AAA CTT CAG CTC AAT TTG GGA CAA GGC CTC AGA ACT
His Ile Gln Asn Ser Lys Leu Gln Leu Asn Leu Gly Gln Gly Leu Arg Thr

      4200        4210        4220        4230        4240
GAC CCC GTC ACC AAC CAG CTG GAA GTG CCC CTC GGT CAA GGT TTG GAA ATT
Asp Pro Val Thr Asn Gln Leu Glu Val Pro Leu Gly Gln Gly Leu Glu Ile

      4250        4260        4270        4280        4290
GCA GAC GAA TCC CAG GTT AGG GTT AAA TTG GGC GAT GGC CTG CAG TTT GAT
Ala Asp Glu Ser Gln Val Arg Val Lys Leu Gly Asp Gly Leu Gln Phe Asp

      4300        4310        4320        4330        4340
TCA CAA GCT CGC ATC ACT ACC GCT CCT AAC ATG GTC ACT GAA ACT CTG TGG
Ser Gln Ala Arg Ile Thr Thr Ala Pro Asn Met Val Thr Glu Thr Leu Trp

      4350        4360        4370        4380        4390
ACC GGA ACA GGC AGT AAT GCT AAT GTT ACA TGG CGG GGC TAC ACT GCC CCC
Thr Gly Thr Gly Ser Asn Ala Asn Val Thr Trp Arg Gly Tyr Thr Ala Pro

      4400        4410        4420        4430        4440
GGC AGC AAA CTC TTT TTG AGT CTC ACT CGG TTC AGC ACT GGT CTA GTT TTA
Gly Ser Lys Leu Phe Leu Ser Leu Thr Arg Phe Ser Thr Gly Leu Val Leu

      4450        4460        4470        4480        4490        4500
GGA AAC ATG ACT ATT GAC AGC AAT GCA TCC TTT GGG CAA TAC ATT AAC GCG
Gly Asn Met Thr Ile Asp Ser Asn Ala Ser Phe Gly Gln Tyr Ile Asn Ala

      4510        4520        4530        4540        4550
GGA CAC GAA CAG ATC GAA TGC TTT ATA TTG TTG GAC AAT CAG GGT AAC CTA
Gly His Glu Gln Ile Glu Cys Phe Ile Leu Leu Asp Asn Gln Gly Asn Leu

      4560        4570        4580        4590        4600
AAA GAA GGA TCT AAC TTG CAA GGC ACT TGG GAA GTG AAG AAC AAC CCC TCT
Lys Glu Gly Ser Asn Leu Gln Gly Thr Trp Glu Val Lys Asn Asn Pro Ser

      4610        4620        4630        4640        4650
GCT TCC AAA GCT GCT TTT TTG CCT TCC ACC GCC CTA TAC CCC ATC CTC AAC
Ala Ser Lys Ala Ala Phe Leu Pro Ser Thr Ala Leu Tyr Pro Ile Leu Asn

      4660        4670        4680        4690        4700
GAA AGC CGA GGG AGT CTT CCT GGA AAA AAT CTT GTG GGC ATG CAA GCC ATA
Glu Ser Arg Gly Ser Leu Pro Gly Lys Asn Leu Val Gly Met Gln Ala Ile

      4710        4720        4730        4740        4750
CTG GGA GGC GGG GGC ACT TGC ACT GTG ATA GCC ACC CTC AAT GGC AGA CGC
Leu Gly Gly Gly Gly Thr Cys Thr Val Ile Ala Thr Leu Asn Gly Arg Arg

      4760        4770        4780        4790        4800
AGC AAC AAC TAT CCC GCG GGC CAG TCC ATA ATT TTC GTG TGG CAA GAA TTC
Ser Asn Asn Tyr Pro Ala Gly Gln Ser Ile Ile Phe Val Trp Gln Glu Phe
```

FIGURE 7-7

```
 4810          482           4830          484           4850
AAC ACC ATA GCC C.. CAA CCT CTG AAC CAC TCT ACA CTT ACT TTT TCT TAC
Asn Thr Ile Ala Arg Gln Pro Leu Asn His Ser Thr Leu Thr Phe Ser Tyr

4860          4870          4880          4890          4900
TGG ACT TA AAT AAG TTG GAA ATA AAG AGT TAA ACT GAA TGT TTA AGT GCA
Trp Thr

4910          4920          4930          4940          4950
ACA GAC TTT TAT TGG TTT TGG CTC ACA ACA AAT TAC AAC AGC ATA GAC AAG

4960          4970          4980          4990          5000
TCA TAC CGG TCA AAC AAC ACA GGC TCT CGA AAA CGG GCT AAC CGC TCC AAG

5010          5020          5030          5040          5050          5060
AAT CTG TCA CGC AGA CGA GCA AGT CCT AAA TGT TTT TTC ACT CTC TTC GGG

              5070          5080          5090          5100
GCC AAG TTC AGC ATG TAT CGG ATT TTC TGC TTA CAC CTT T
```

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FIGURE 7-8

```
Ad2     MSKEIPTPYMWSYQPQMGLAAGAAQDYSTRINYMSAGPHMISRVNGIRAH   50

BAV3        LIKQPVVGTTHV----------------------EMPRNEVLEQH   23
            :. :   . ::                      .::     :
Ad2     RNRILLEQAAITTTPRNNLNPRSWPAALVYQESPAPTTVVLPRDAQAEVQ  100

BAV3    LTSHGAQIAGGG-----AAGDYFKSPTSARTLIPLTASCL------RPDG   62
        .:  :::.:::      . :          : :    .       ::::
Ad2     MTNSGAQLAGGFRHRVRSPGQGITHLKIRGRGIQLNDESVSSSLGLRPDG  150

BAV3    VFQLGGGSRSSFNPLQTDFAFHALPSRPRHGGIGSRQFVEEFVPAVYLNP  112
         ::.::  :::: : :.  .  .  : :: ::::. ::.::::::.:: ::
Ad2     TFQIGGAGRSSFTPRQAILTLQTSSSEPRSGGIGTLQFIEEFVPSVYFNP  200

BAV3    YSGPPDSYPDQFIRHYNVYSNSVSGYS  139
        .::::  ::::::  .     :  ::
Ad2     FSGPPGHYPDQFIPNFDAVKDSADGYD  227
```

FIGURE 8(a)

```
BAV3    M------EPDGVHAEQQFILNQISCANTALQRQREELASLVMLHACKRGL   77
        :      : ::. .::  .     : .  ::   ::  .: :: :::::.
Ad5     MTDTLDLEMDGIITEQRLL--ERRRAAAEQQRMNQELQDMVNLHQCKRGI   48

BAV3    FCPVKTYKLSLNASASEHSLHFEKSPSRFTLVNTHAGASVRVALHHQGAS  127
        :: ::  :.. . .. : : .     :  ::       . .. :   .
Ad5     FCLVKQAKVTYDSNTTGHRLSYKLPTKRQKLVVMVGEKPITITQHSVETE   98

BAV3    GSIRCSCSHAECLPVLLKTLCAFNFLD     154
        : :   :   : :  :.::::   :
Ad5     GCIHSPCQGPEDLCTLIKTLCGLKDLIPFN  128
```

Sheet 20 of 33 - Drawings - As Filed

FIGURE 8(b)

BAV3 - MKRSVPQD--FNLVYPYKAKR-----PNIMPPFFDRNGFVENQEATLAML -43
Ad2 - MKRARPSEDTFNPVYPYDTETGPPTVPFLTPPFVSPNGFQESPPGVLSLR -50
BAV3 - VEKPLTFDKE-GALTLGVGRGIRINPAGLLETNDLASAVFPPLASDEAGN -92
Ad2 - VSEPL--DTSHGMLALKMGSGLTLDKAGNLTSQNVTTV---------- -86
BAV3 - VTLNMSDGLYTKDNKLAVKVGPGLSLDSNNALQVHTGDGLTVTDDKVSLN -142
Ad2 - -----TQPLKKTKSNISLDTSAPLTI-TSGALTVATTAPLIVTSGALSVQ -130
BAV3 - TQAPLSTTSAGLSLLLGPSLHLGEEERLTVNTGAGLQISNNALAVKVGSG -192
Ad2 - SQAPLT----------VQDSKLSIATKGPITVSDGKLALQTSAP -164
BAV3 - ITVDAQNQLAASLGDGLESRDNKTVVKAGPGLTITNQALTVATGNGLQVN -242
Ad2 - LSGSDSDTLTVT----------ASPPLTTATGS-LGIN -191
BAV3 - PEGQLQLNITAGQGLNFANNSLAVELGSGLHFPPGQNQVSLYPGDGIDIR -292
Ad2 - MEDPIYVN----------NGKIGIKISGPLQVAQ---------- -215
BAV3 - DNRVTVPAGPGLRMLNHQLAVASGDGLEVHSDTLRLKLSHGLTFENGAVR -342
Ad2 - ----------NSDTLTVVTGPGVTVEQNSLR -236
BAV3 - AKLGPGLGTDDSGRSVVRTGRGLRVANGQVQIFSGRGTAIGTDSSLTLNI -392
Ad2 - TKVAGAIGYDSSNNMEIKTGGGMRINNNL--LILDVDYPFDAQTKLRLKL -284
BAV3 - RAPLQFSGPALTASLQGSGPITYNSNNGTFGLSIGPGMWVDQNRLQVNPG -442
Ad2 - ----------GQGPLYINASHN----------LDINYN -302
BAV3 - AGLVFQGNNLVPNLADPLAISDSKISLSLGPGLTQASNALTLSLGNGLEF -492
Ad2 - RGLYL----------FNASNNTKKLEVSIKKSS---------GLNF -329
BAV3 - SNQAVAIKAGRGLRFESSSQALESSLTVGNGLTLTDTVIRPNLGDGLEVR -542
Ad2 - DNTAIAINAGKGLEFDTNT---------- -348
BAV3 - DNKIIVKLGANLRFENGAVTAGTVNPSAPEAPPTLTAEPPLRASNSHLQL -592
Ad2 - ---------- -348
BAV3 - SLSEGLVVHNNALALQLGDGMEVNQHGLTLRVGSGLQMRDGILTVTPSGT -642
Ad2 - ----------SESPDIN--PIKTKIGSGID-------YNENGA -372

FIGURE 8(c)-1

```
BAV3   - PIEPRLTAPLTQTENGIGLALGAGLELDESALQVKVGPGMRLNPVEKYVT -692
Ad2    - MIT----------------KLGAGLSFDNSG------------------- -387

BAV3   - LLLGPGLSFGQPANRTNYDVRVSVEPPMVFGQRGQLTFLVGHGLHIQNSK -742
Ad2    - -----AITIG-----NKNDDKLTLWTTPDPSP---------------NCR -412

BAV3   - LQLNLGQGLRTDPVTNQLEVPLGQGLEIADESQVRVKLGDGLQFDSQARI -792
Ad2    - IHSD-------------------------NDCKFTLVLT---KCGSQVLA -434

BAV3   - TTAPNMVTETLWTGTGSNANVTWRGYTAPGSKLFLSLTRFSTGLVLGNMT -842
Ad2    - TVAALAVSGDLSSMTGTVASVS----------IFLRFDQ--NGVLMENSS -472

BAV3   - IDSNASFGQYINAGHEQIECFILLDNQGNLKEGSNLQGTWEVKNNPSASK -892
Ad2    - LKKHY----------------------WNFRNGNS------TNANPYTNA -494

BAV3   - AAFLPSTALYPILNESRGSLPGKNLVGMQAILGGGGTCTVIA-TLNGRRS -941
Ad2    - VGFMPNLLAYP---KTQSQTAKNNIVSQVYLHGDKTKPMILTITLNGTSE -541

BAV3   - NNYPAGQSII---FVWQ-EFNTIARQPLNHSTLTFSYWT -976
Ad2    - STETSEVSTYSMSFTWSWESGKYTTETFATNSYTFSYIAQE -582
```

FIGURE 8(c)-2

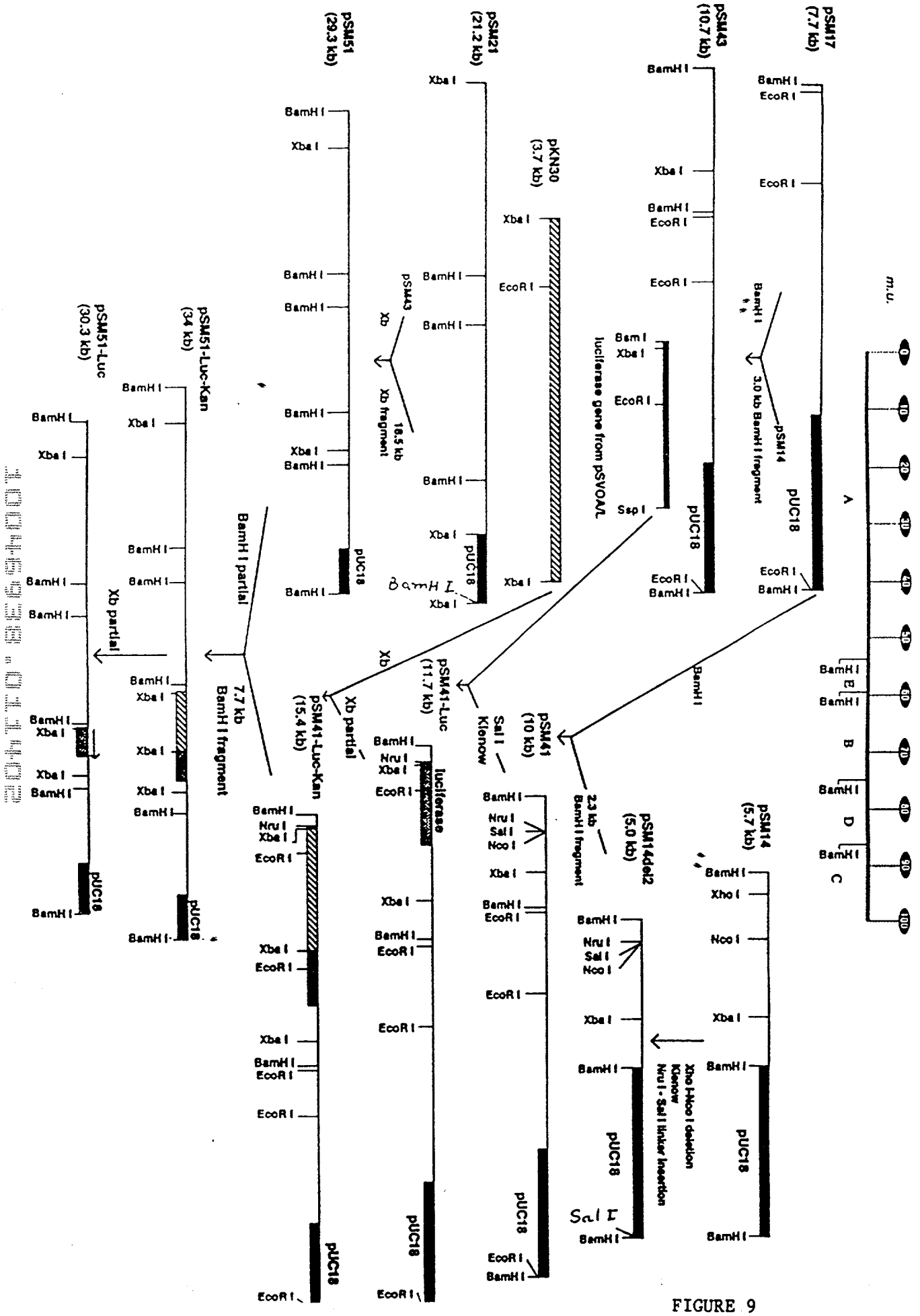

pSM51 (29.3 kb)
pSM21 (21.2 kb)
pKN30 (3.7 kb)
pSM43 (10.7 kb)
pSM17 (7.7 kb)
pSM51-Luc (30.3 kb)
pSM51-Luc-Kan (34 kb)
pSM41-Luc-Kan (15.4 kb)
pSM41-Luc (11.7 kb)
pSM41 (10 kb)
pSM14del2 (5.0 kb)
pSM14 (5.7 kb)
luciferase gene from pSVOAL
luciferase
BamH I partial
Xb partial
7.7 kb BamH I fragment
18.5 kb Xb fragment
3.0 kb BamH I fragment
2.3 kb BamH I fragment
Sal I Klenow
Xho I-Nco I deletion Klenow Nru I - Sal I linker insertion
pUC18
m.u.
A
B
C
D
E

FIGURE 9

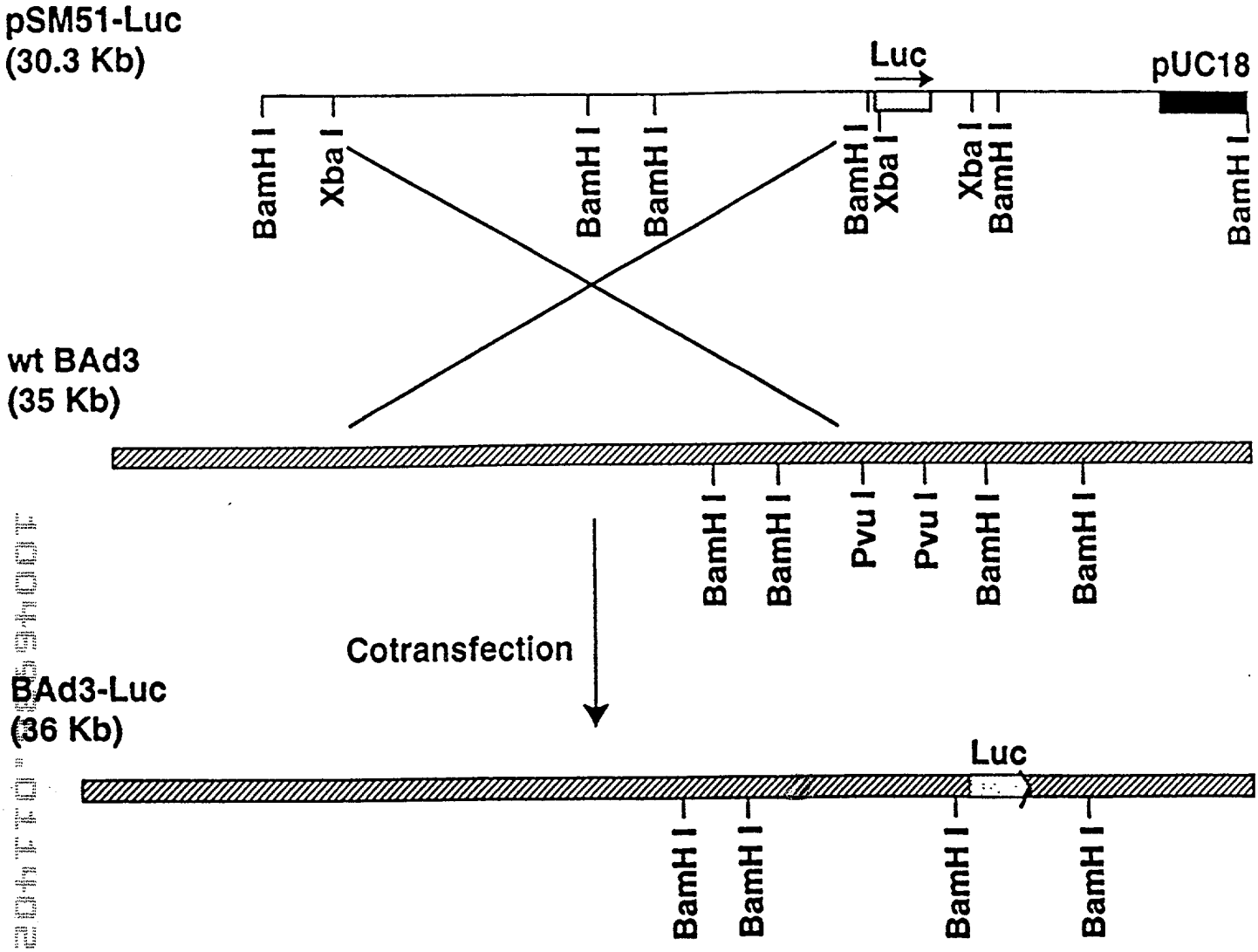
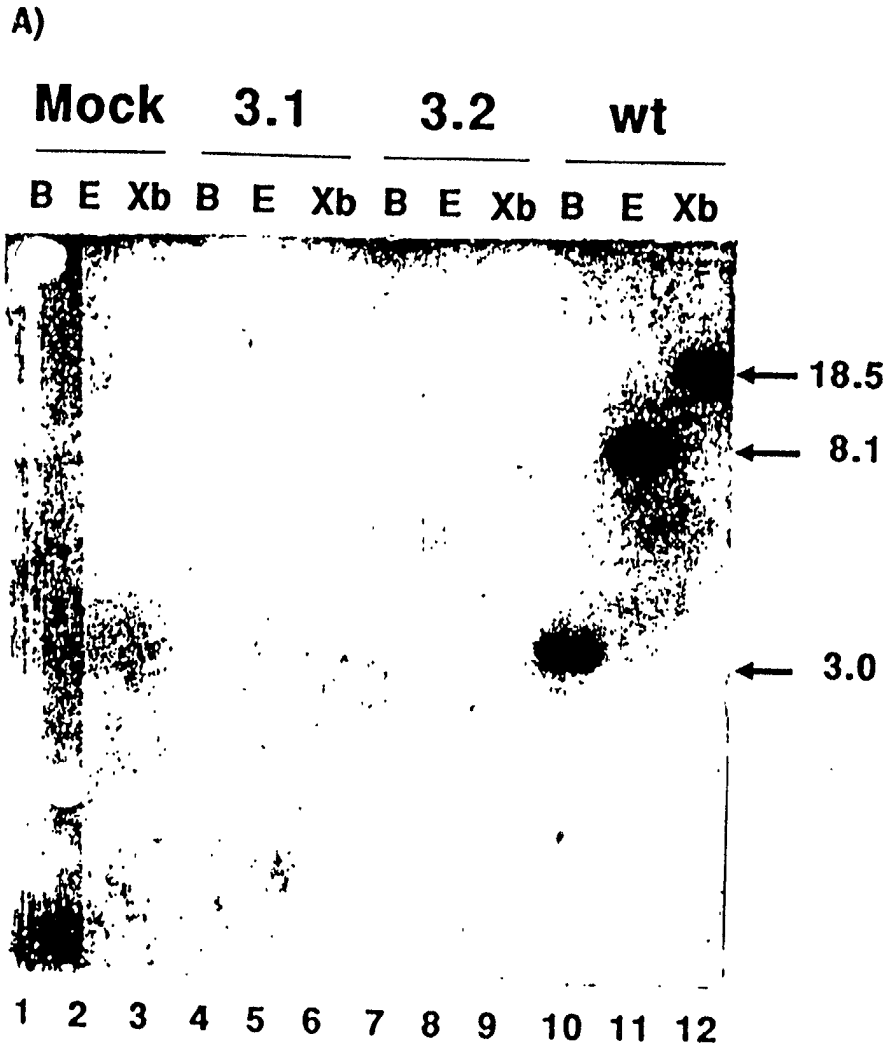

pSM51-Luc
(30.3 Kb)
Luc
pUC18
BamH I
Xba I
BamH I
BamH I
BamH I
Xba I
Xba I
BamH I
BamH I
wt BAd3
(35 Kb)
BamH I
BamH I
Pvu I
Pvu I
BamH I
BamH I
Cotransfection
BAd3-Luc
(36 Kb)
Luc
BamH I
BamH I
BamH I
BamH I

FIGURE 10

20hTTO" 8E69h00T

Title: RECOMBINANT PROTEIN PRODUCTION IN BOVINE ADENOVIRUS EXPRESSION VECTOR SYSTEM
Inventor: Suresh K. MITTAL et al.
Application No.: To Be Assigned
Docket No.: 29310200210 3
Sheet 25 of 33



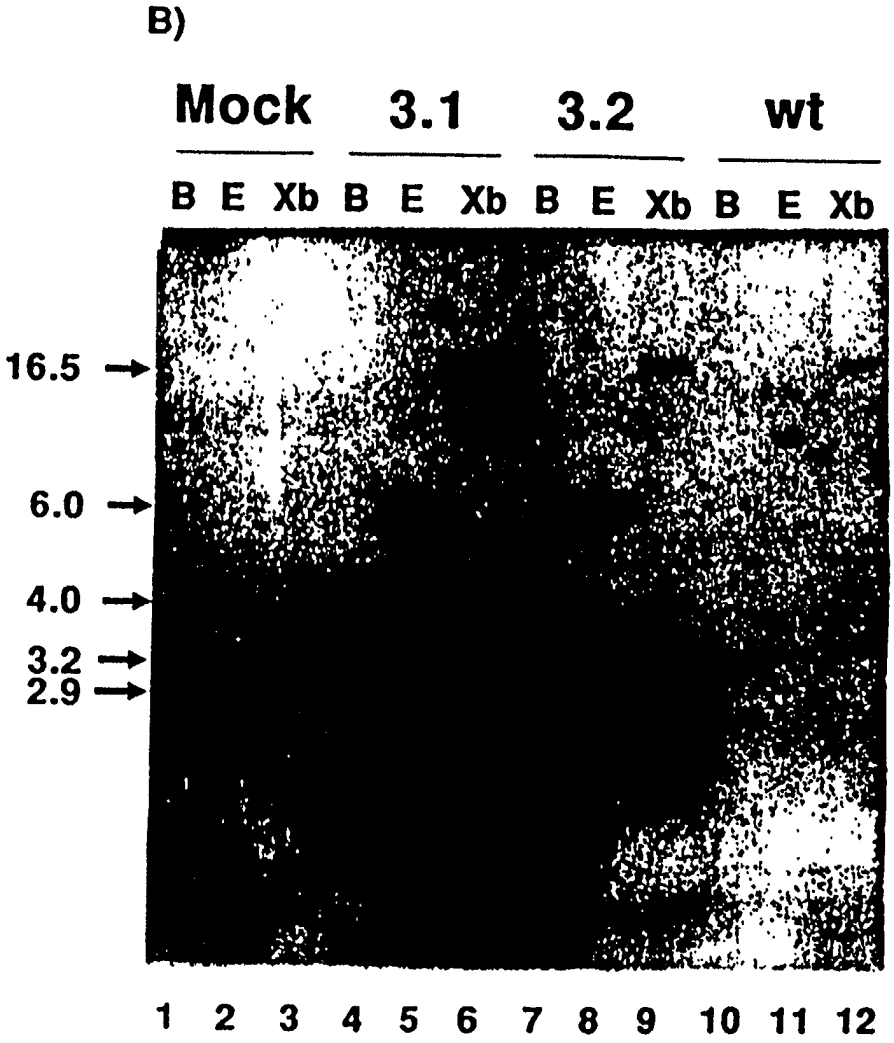


FIGURE 11

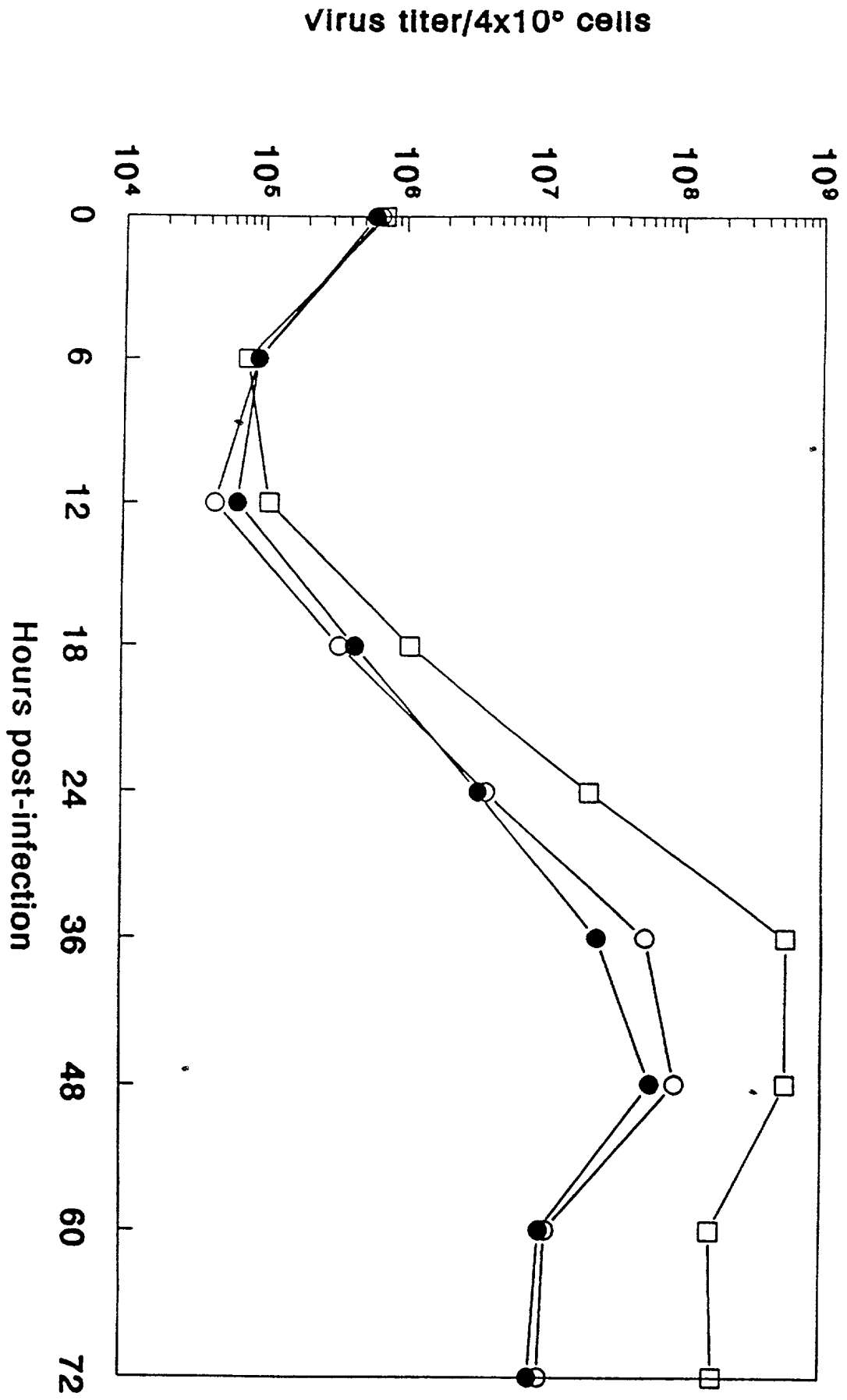

Virus titer/4x10⁶ cells
10⁴
10⁵
10⁶
10⁷
10⁸
10⁹
0
6
12
18
24
36
48
60
72
Hours post-infection
wt
3.1
3.2

FIGURE 12

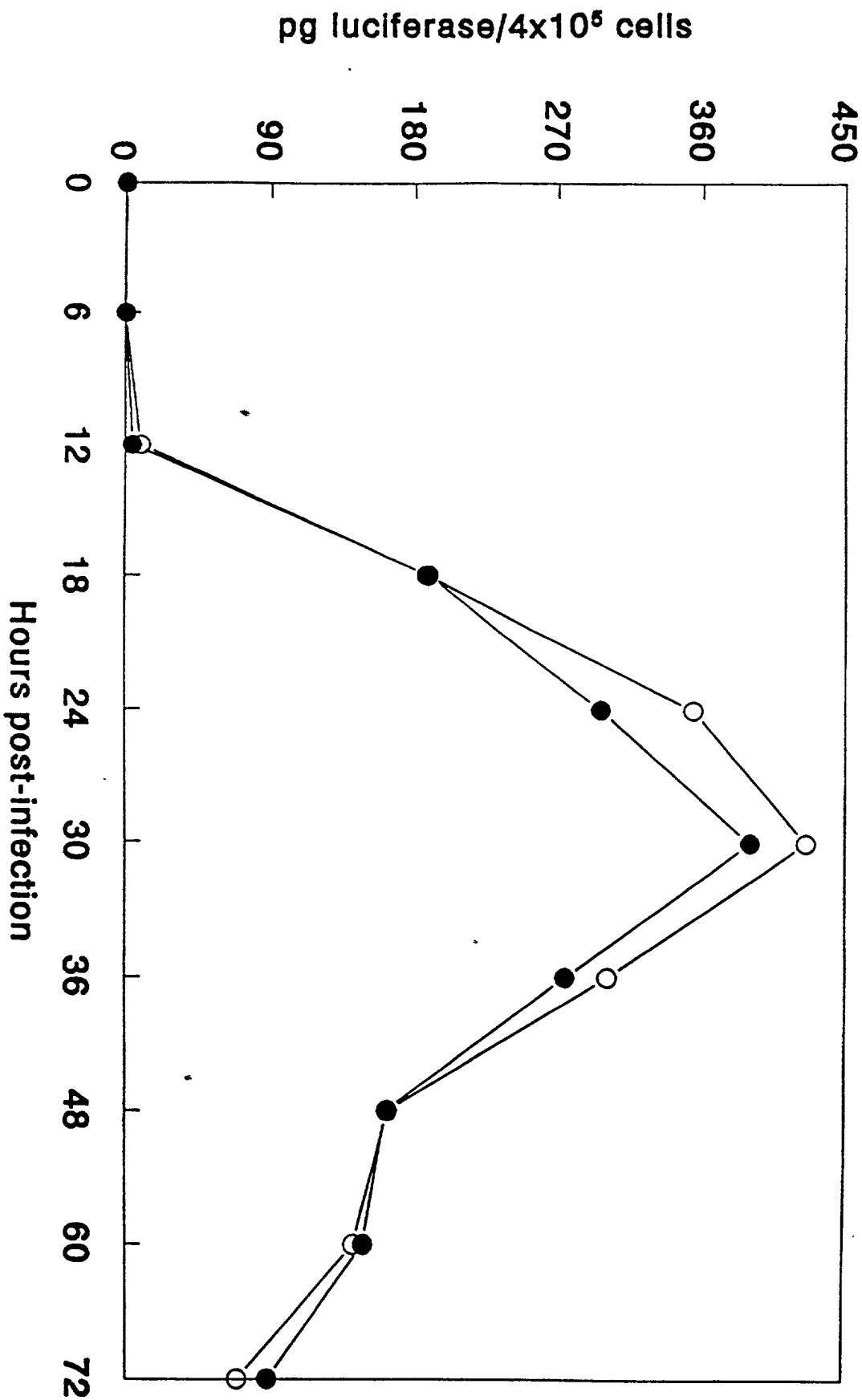
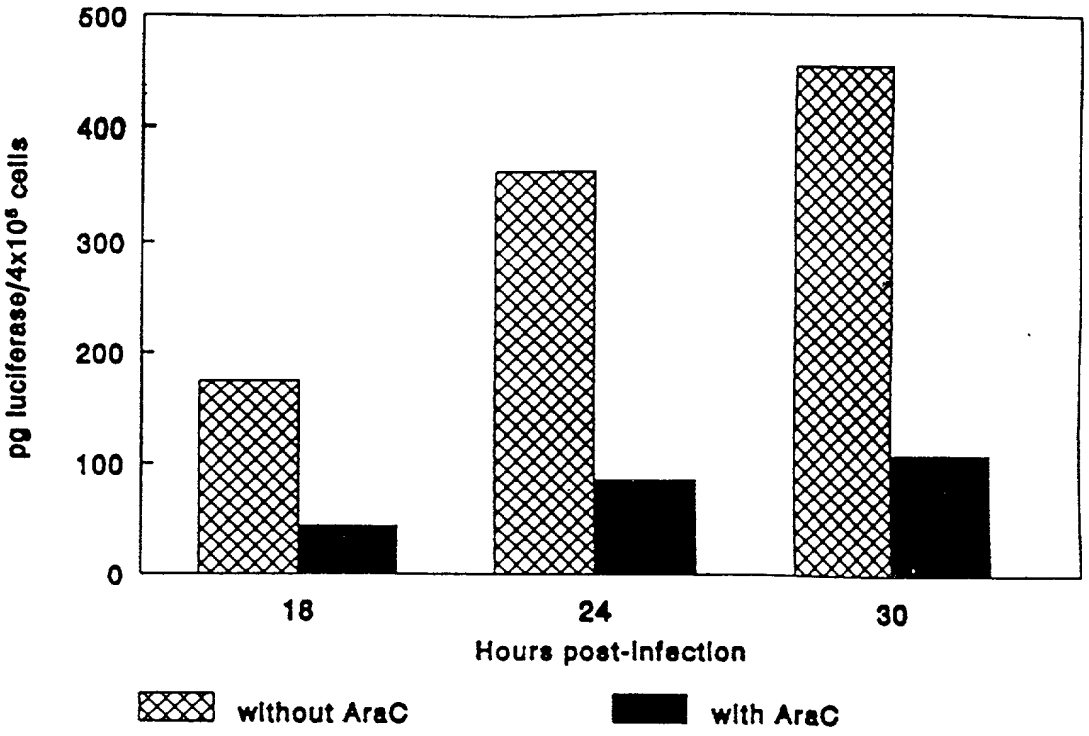


FIGURE 13

20170.0.85.84001

A)


500
400
300
200
100
0
pg luciferase/4x10⁵ cells
18
24
30
Hours post-Infection
without AraC
with AraC

B)

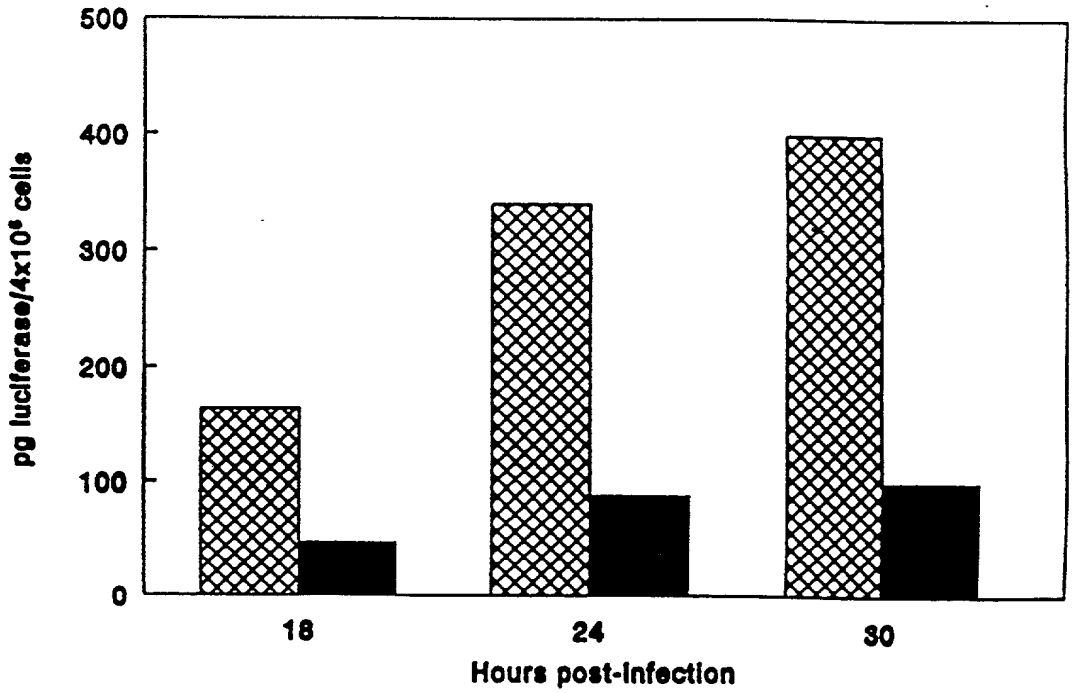

500
400
300
200
100
0
pg luciferase/4x10⁵ cells
18
24
30
Hours post-Infection

FIGURE 14

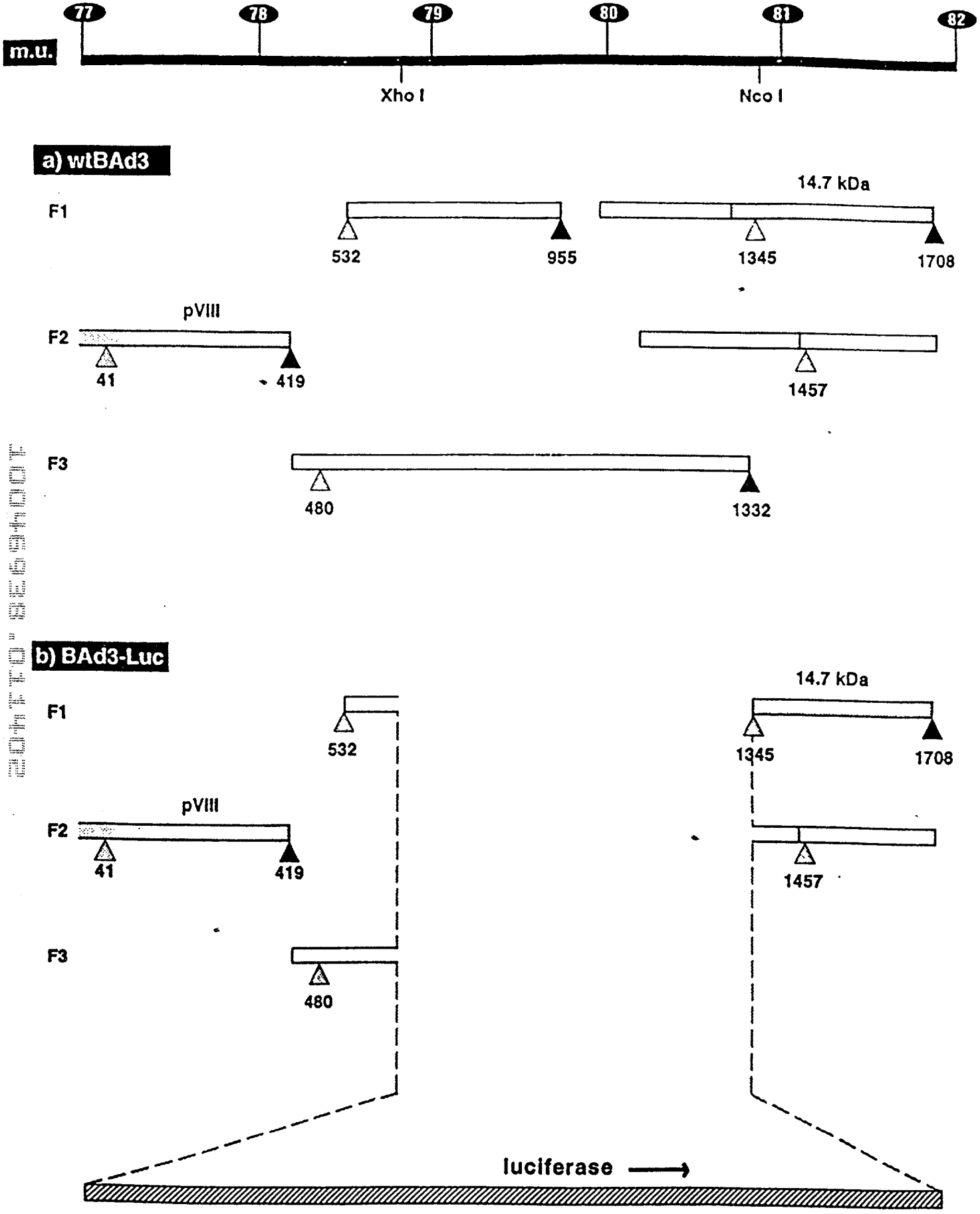

77
78
79
80
81
82
m.u.
Xho I
Nco I
a) wtBAd3
F1
532
955
14.7 kDa
1345
1708
pVIII
F2
41
419
1457
F3
480
1332
b) BAd3-Luc
F1
532
14.7 kDa
1345
1708
pVIII
F2
41
419
1457
F3
480
luciferase

FIGURE 15

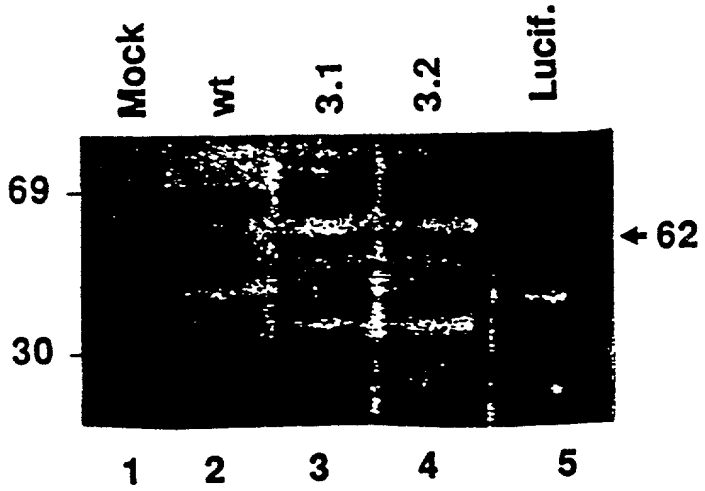


FIGURE 16

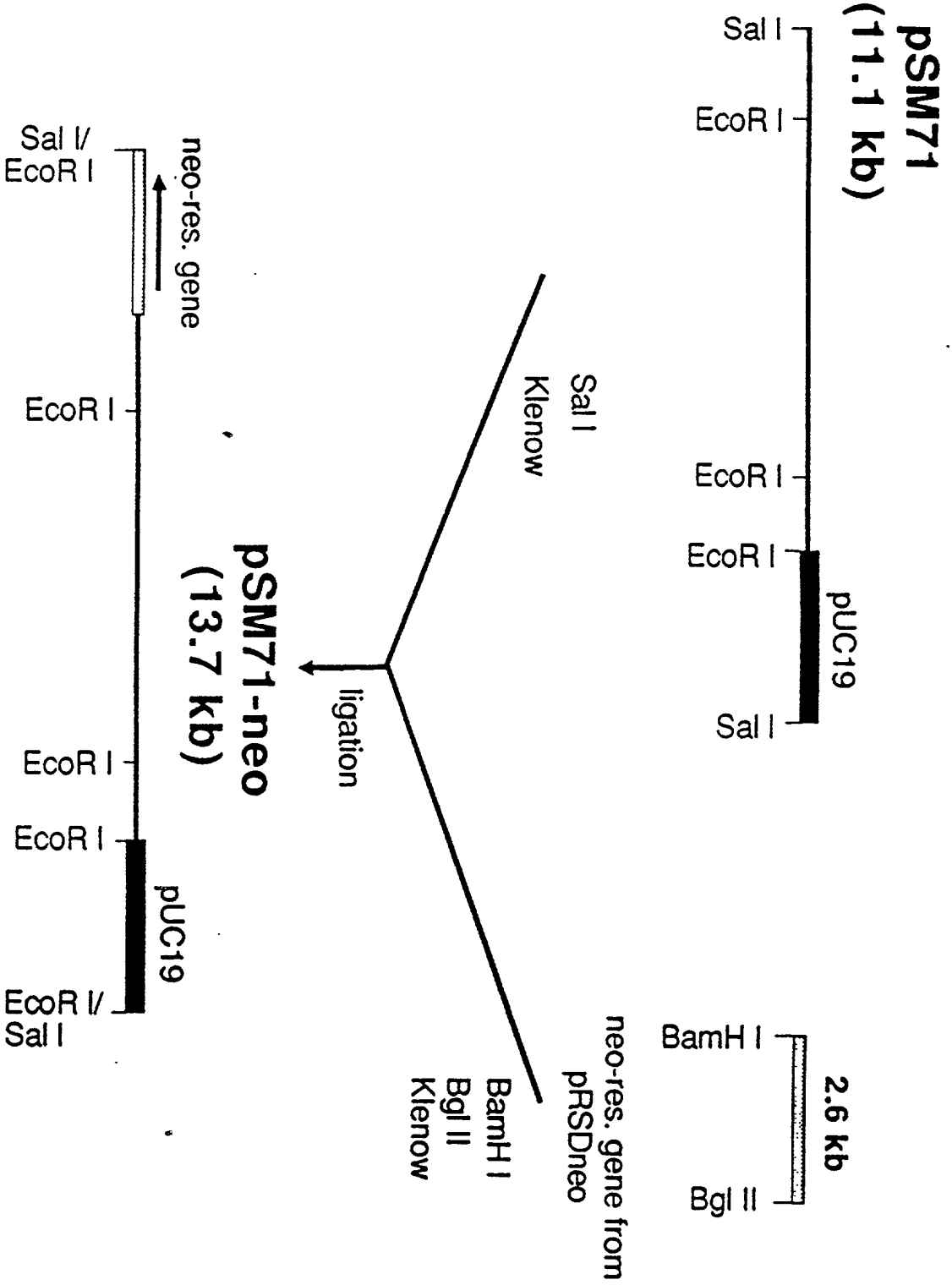

pSM71
(11.1 kb)
Sal I
EcoR I
EcoR I
EcoR I
pUC19
Sal I
Sal I
Klenow
ligation
Sal I/
EcoR I
neo-res. gene
EcoR I
pSM71-neo
(13.7 kb)
EcoR I
EcoR I
pUC19
EcoR I/
Sal I
BamH I
Bgl II
Klenow
neo-res. gene from
pRSDneo
BamH I
2.6 kb
Bgl II

FIGURE 17

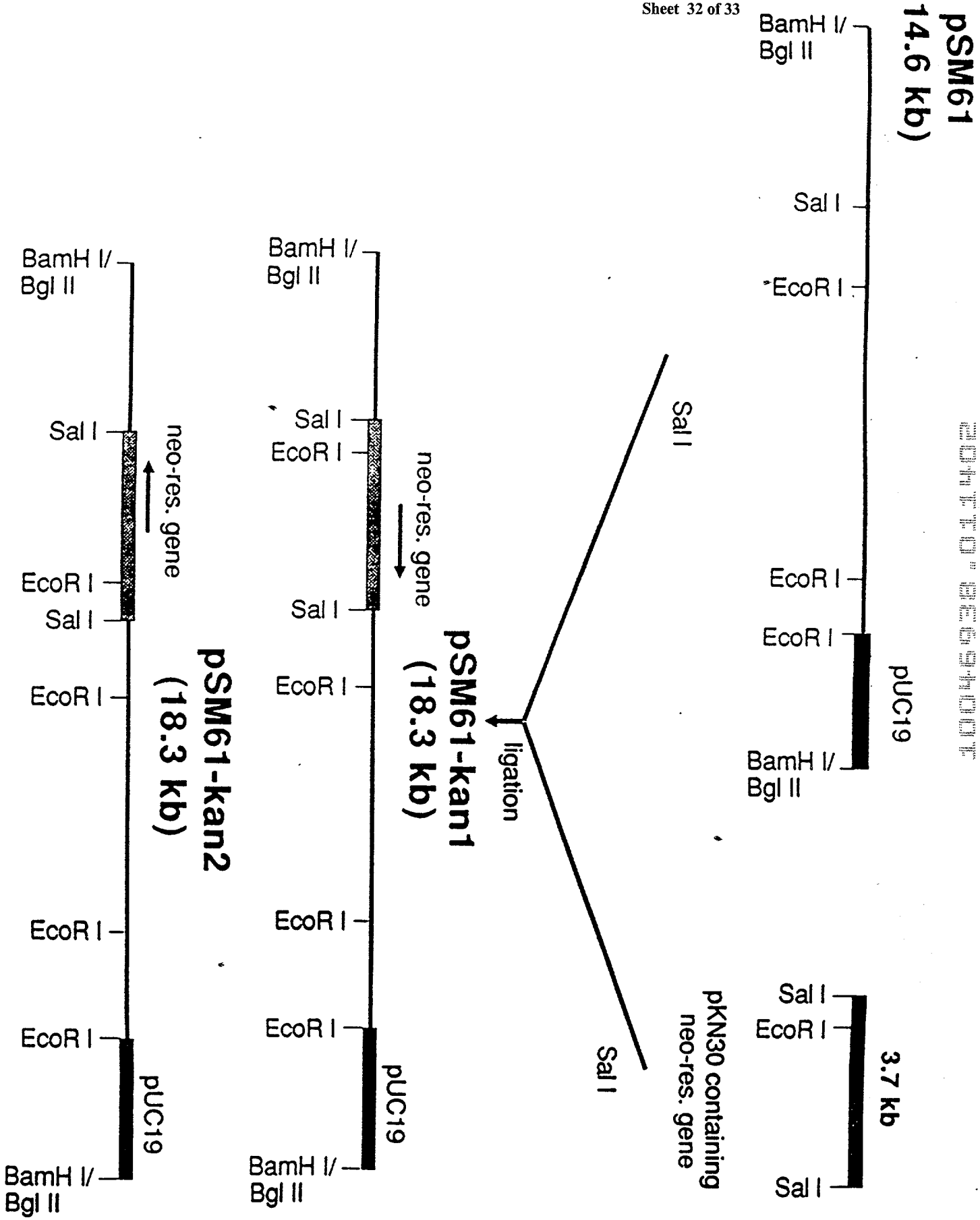

pSM61
(14.6 kb)
BamH I/
Bgl II
Sal I
EcoR I
EcoR I
pUC19
BamH I/
Bgl II
Sal I
EcoR I
neo-res. gene
Sal I
EcoR I
pSM61-kan1
(18.3 kb)
EcoR I
EcoR I
pUC19
BamH I/
Bgl II
ligation
Sal I
pKN30 containing
neo-res. gene
Sal I
Sal I
EcoR I
3.7 kb
Sal I
BamH I/
Bgl II
Sal I
neo-res. gene
EcoR I
Sal I
pSM61-kan2
(18.3 kb)
EcoR I
EcoR I
pUC19
BamH I/
Bgl II

FIGURE 18

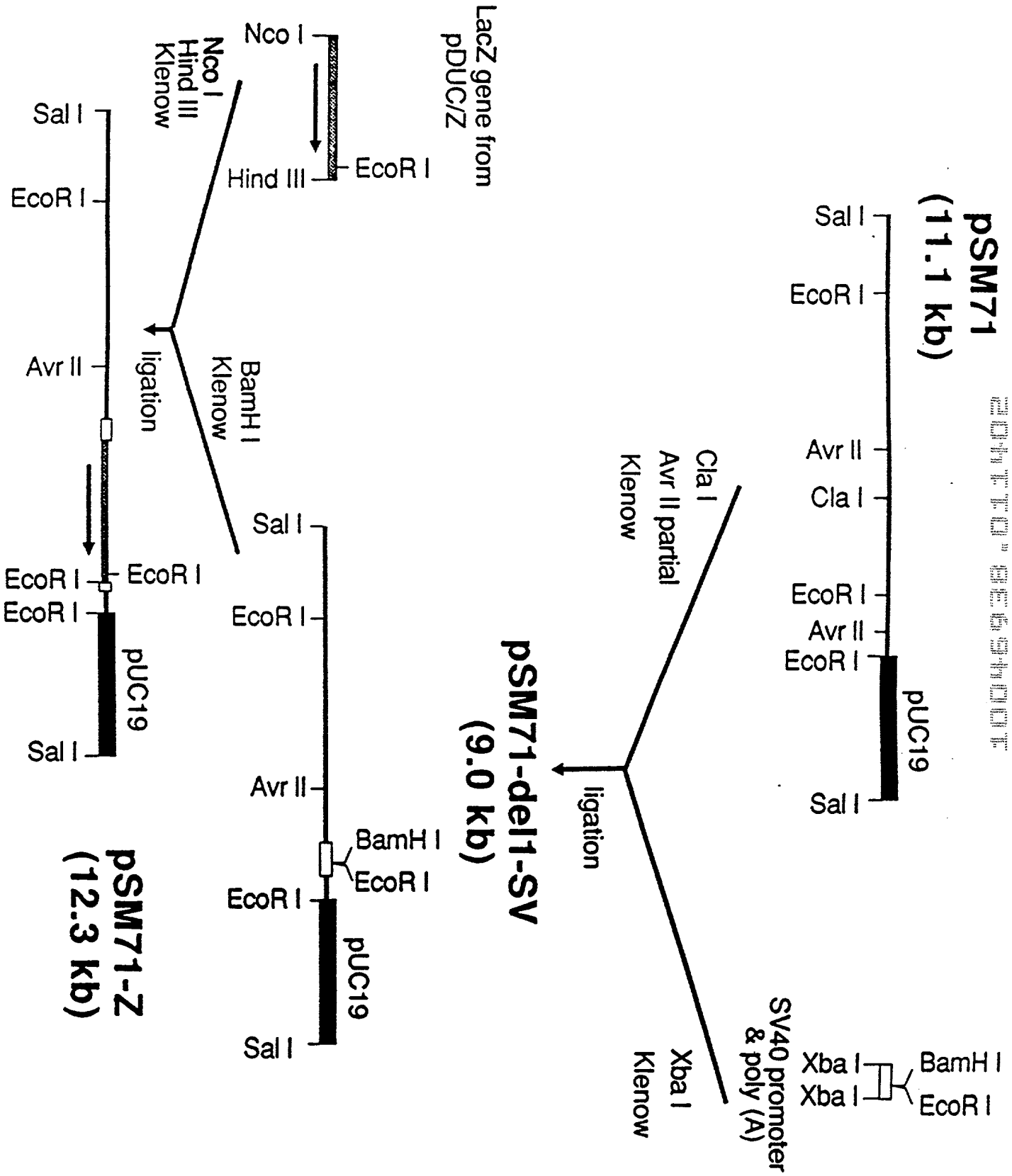

Nco I
Hind III
Klenow
Sal I
EcoR I
Avr II
ligation
BamH I
Klenow
LacZ gene from pDUC/Z
Hind III
EcoR I
EcoR I
EcoR I
EcoR I
pUC19
Sal I
pSM71-Z (12.3 kb)
Sal I
EcoR I
Avr II
BamH I
EcoR I
EcoR I
pUC19
Sal I
pSM71-del1-SV (9.0 kb)
Cla I
Avr II partial
Klenow
ligation
Xba I
Klenow
SV40 promoter & poly (A)
Xba I
Xba I
BamH I
EcoR I
pSM71 (11.1 kb)
Sal I
EcoR I
Avr II
Cla I
EcoR I
Avr II
EcoR I
pUC19
Sal I

FIGURE 19